

SEQUENCE LISTING

000000-0000-0000-0000-000000000000
DRAFT--00000000000000000000000000000000

<110> Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.

<120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

<130> 10466-14

<140> 09/665,350
<141> 2000-09-18

<150> PCT/US00/04414
<151> 2000-02-22

<150> US 60/143,048
<151> 1999-07-07

<150> US 60/145,698
<151> 1999-07-26

<150> US 60/146,222
<151> 1999-07-28

<150> PCT/US99/20594
<151> 1999-09-08

<150> PCT/US99/20944
<151> 1999-09-13

<150> PCT/US99/21090
<151> 1999-09-15

<150> PCT/US99/21547
<151> 1999-09-15

<150> PCT/US99/23089
<151> 1999-10-05

<150> PCT/US99/28214
<151> 1999-11-29

<150> PCT/US99/28313
<151> 1999-11-30

<150> PCT/US99/28564
<151> 1999-12-02

<150> PCT/US99/28565
<151> 1999-12-02

<150> PCT/US99/30095
<151> 1999-12-16

<150> PCT/US99/30911
<151> 1999-12-20

<150> PCT/US99/30999
<151> 1999-12-20
<150> PCT/US00/00219
<151> 2000-01-05

<160> 423

<210> 1
<211> 1825
<212> DNA
<213> Homo sapiens

<400> 1
actgcacctc gtttctatcg attgaattcc cggggatcc tctagagatc cctcgaccc 60
gaccacgcg tccgggccc agcagcacgg cgcaggacc tggagctccg gtcgcgttt 120
ccgcagcgc tacccgcatt gcgcctgcgc cgccggggccg cgctggggct cctgccgtt 180
ctgctgtgc tgccggccgc gccggaggcc gccaagaagc cgacgcctg ccacgggtgc 240
cgggggctgg tggacaaggta acccagggg atggtgacca ccgcaaagaa gaactttggc 300
ggcggaaca cggcttggga ggaaaagacg ctgtccaagt acgagtccag cgagattcgc 360
ctgctggaga tcctggagg gctgtgcgag agcagcgaact tcgaatgcaa tcagatgcta 420
gaggcgcagg aggagcacct ggaggcctgg tggctgcagc tgaagagcga atatcctgac 480
ttattcgagt gttttgtgt gaagacactg aaagtgtgt gcttcagg aacctacgg 540
cccactgtc tcgcatgcca gggcggatcc cagaggccct gcagcgggaa tggccactgc 600
agcggagatg ggagcagaca gggcgcacggg tcctgcgggt gccacatggg gtaccaggc 660

ccgctgtgca ctgactgcat ggacggctac tttagtgcg tccggAACGA gaccCACAGC 720
atctgcacag cctgtgacga gtcctgcaag acgtgctcg gcctgACCAA cagAGACTGC 780
ggcggAGTG aagtgggCTG ggtgctggac gagGGCGCT gtgtggATGT ggacgAGTGT 840
gcggccgAGC cgccTCCCTG cagcgtgCG cagttCTGta agaacGCCAA cggctccTAC 900
acgtgcGAAG agtgtgACTC cagctgtGT ggctgcACAG gggAAggCCC aggAAactGT 960
aaagagtGTA tctctggCTA cgcgaggGGAG cacggACAGT gtgcAGATGT ggacgAGTGC 1020
tcactagcAG aaaaaacCTG tgtgaggAAA aacgAAAact gctacaatac tccaggGGAGC 1080
tacgtctGTG tgtgtccTGA cggcttcGAA gaaaACGGAA atgcctgtGT gccggcGGCA 1140
gaggctGAAG ccacagaAGG agaaaAGCCC ACACAGCTGC cttccCGCA agacCTGTA 1200
tgtgccggAC ttaccCTTA aattattTCAG aaggatgtCC cgtggAAAAT gtggccCTGA 1260
ggatgccGTC tcctgcAGTG gacagGGCG gggagAGGCT gcctgctCTC taacggTTGA 1320
ttctcattTG tcccttaAAC agctgcATT CTTGGTTGT CTTAAACAGA CTTGTATATT 1380
ttgatacAGT tctttgtAAAT aaaattGACC attgtAGGTA atcaggAGGA aaaaaaaaaaa 1440
aaaaaaaaaaa aaaggGCGC CGCGACTCTA gagTCGACCT gcagaAGCTT ggccGCCATG 1500
gcccaactTG tttattGcAG cttataatGG ttacaAAATAA agcaatAGCA tcacAAATT 1560
cacaAAataAA gcattttttt cactgcATTc tagttgtGGT ttgtccAAAC tcataatGT 1620
atcttatCAT gtctggATCG ggaattaATT cggcgcAGCA ccatgcCTG aaataACCTC 1680
tgaaagAGGA acttggTTAG gtaccttCTG aggCGGAAAG aaccAGCTGT ggaatgtGTG 1740
tcagtttagGG tggaaaAGT ccccAGGCTC cccAGCAGGC agaagtATGC aagcatGCAT 1800
ctcaattAGT cagcaacCCA gtttt 1825

<210> 2

<211> 353

<212> PRT

<213> Homo sapiens

<400> 2

Met Arg Leu Pro Arg Arg Ala Ala Leu Gly Leu Leu Pro Leu Leu Leu
1 5 10 15

Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro Cys His
20 25 30

Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
 35 40 45

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
 50 55 60

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
65 70 75 80

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
 85 90 95

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
 100 105 110

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
 115 120 125

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
 130 135 140

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
 145 150 155 160

Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
 165 170 175

Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
 180 185 190

His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
 195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
 210 215 220

Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
 225 230 235 240

Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
 245 250 255

Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
 260 265 270

Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
 275 280 285

Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys
 290 295 300

Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
 305 310 315 320

Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala
 325 330 335

Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp
 340 345 350

Leu

<210> 3

<211> 2206

<212> DNA

<213> Homo sapiens

<400> 3

caggtccaac tgcacacctgg ttctatcgat tgaattcccc gggatcctc tagagatccc 60
 tcgacctcga cccacgcgtc cgccaggccg ggaggcgacg cgcccgccg tctaaacggg 120
 aacagccctg gctgagggag ctgcagcgca gcagagtatac tgacggcgcc aggttgcgta 180
 ggtgcggcac gaggagttt cccggcagcg aggaggtcct gagcagcatg gcccggagga 240

gccccttccc tggcgcgcg ctctggctct ggagcatccct cctgtgcctg ctggcactgc 300
ggcgaggc cggccgcgcg caggaggaga gcctgtacct atggatcgat gtcaccagg 360
caagactact cataggattt gaagaagata tcctgattgt ttcaaggaaa aaaatggcac 420
ctttacaca tgatttcaga aaagcgcac agagaatgcc agcttccct gtcaatattcc 480
atccatgaa ttttacctgg caagctgcag ggcaggcaga atacttctat gaattcctgt 540
ccttcgcctc cctggataaa ggcatcatgg cagatccac cgtcaatgtc cctctgctgg 600
gaacagtgcc tcacaaggca tcagttgttc aagttggttt cccatgtctt gaaaaacagg 660
atggggtggc agcatttgaa gtggatgtga ttgttatgaa ttctgaaggc aacaccatcc 720
tccaaacacc tcaaaatgct atcttcctta aaacatgtca acaagctgag tgcccaggcg 780
ggtgcgaaa tggaggctt tgtaatgaaa gacgcacatcg cgagtgtcct gatgggttcc 840
acggacctca ctgtgagaaa gccctttgtc ccccacgtat tatgaatggt gactttgtg 900
tgactcctgg tttctgcata tgcccacctg gattctatgg agtgaactgt gacaaagcaa 960
actgctcaac cacctgcctt aatggaggga cctgtttcta ccctggaaaa ttttgcctt 1020
ctccaggact agagggagag cagtgtgaaa tcagcaaattt cccacaaccc tgtcgaaatg 1080
gaggtaaatg cattggtaaa agcaaattgt aagtgttccaa aggttaccag ggagacctct 1140
gttcaaagcc tggctgcag cctggctgtg gtgcacatgg aacctgcctt gaacccaaca 1200
aatgccaatg tcaagaaggt tggcatggaa gacactgcaaa taaaaggtaa gaagccagcc 1260
tcatacatgc cctgaggcca gcaggcgccc agtcaggca gcacacgcct tcacttaaaa 1320
aggccgagga gcccgggat ccacctgaat ccaattacat ctggtaact ccgacatctg 1380
aaacgttttta agttacacca agttcatagc ctttgttaac ctttcatgtg ttgaatgtc 1440
aaataatgtt cattacactt aagaatactg gcctgaattt tattagctt attataaattc 1500
actgagctga tatttactct tccttttaag tttcttaagt acgtctgttag catgatggta 1560
tagattttct tggttcagtg cttgggaca gattttataat tatgtcaattt gatcaggta 1620
aaattttcag tggtagttg gcagatattt tcaaaaattac aatgcatttta tgggtctgg 1680
gggcaggaaa acatcagaaaa ggttaaattt ggcacaaaatg cgtaagtcac aagaattttg 1740
atggtgcaagt taatgttgc gttacagcat ttcaagatattt attgtcaatg atttagatgt 1800
ttgttacatt ttaaaaattt gctcttaatt tttaaactct caatacaata tattttgacc 1860
ttaccattat tccagagatt cagtattttttt aaaaaaaaaaa ttacactgtg gtatggcat 1920
ttaaaacaata taatataattt taaacacaat gaaataggaa atataatgtt tgaacttttt 1980
gcattggctt gaagcaatataat aatataattgt aaacaaaaca cagctttac ctaataaaaca 2040
ttttatactg tttgtatgtt taaaataaaag gtgtctgtt agtttttgg aaaaaaaaaaa 2100
aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa gggcggccgc gactcttagag tcgacactgca 2160
gaagcttggc cggccatggcc caacttgcattt attgcagctt ataatgt 2206

<210> 4

<211> 379

<212> PRT

<213> Homo sapiens

<400> 4

```

Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser
   1           5           10          15

```

Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln
 20 25 30

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

65	70	75	80
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln			
85	90	95	
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly			
100	105	110	
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro			
115	120	125	
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln			
130	135	140	
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu			
145	150	155	160
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr			
165	170	175	
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys			
180	185	190	
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His			
195	200	205	
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys			
210	215	220	
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn			
225	230	235	240
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys			
245	250	255	
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln			
260	265	270	
Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys			
275	280	285	
Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu			
290	295	300	
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys			
305	310	315	320
His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His			
325	330	335	
Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala			
340	345	350	

SEQUENCE DRAFT

Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Ala Glu Glu
355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
370 375

<210> 5

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 5

agggagcacg gacagtgtgc agatgtggac gagtgctcac tagca

45

<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 6

agagtgtatc tctggctacg c

21

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 7

taagtcggc acattacagg tc

22

<210> 8

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 8

cccacatgt atgaatggtg gactttgtgt gactcctggc ttctgcata

49

<210> 9
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 9
 aaagacgcat ctgcgagtgt cc 22

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 10
 tgctgatttc acactgctct ccc 23

<210> 11
 <211> 2197
 <212> DNA
 <213> Homo sapiens

<400> 11
 cggacgcgtg ggcgtccggc ggtcgcaagag ccaggaggcg gagggcgcg ggccagcctg 60
 ggccccagcc cacacccca ccagggccca ggagccacca tgtggcgatg tccactgggg 120
 ctactgctgt tgctgccgtt ggctggccac ttggctctgg gtgcggcagca gggtcgtggg 180
 cgccggggagc tagcacccggg tctgcacccgt cggggcatcc gggacgcggg agggcggtac 240
 tgccaggaggc aggacctgtg ctgcgcggc cgtgcgcacg actgtgcctt gccctaccc 300
 ggcgcacatct gttactgtga cctttctgc aaccgcacgg tctccgactg ctgcacctgac 360
 ttctgggact tctgcctcg cgtgccaccc cctttcccc cgtatccaagg atgtatgcat 420
 ggaggtcgta tctatccagt cttggaaacg tactgggaca actgtAACCG ttgcacctgc 480
 caggagaaca ggcgtggca tggggatcc agacatgatc aaagccatca accaggggcaa 540
 ctatggctgg caggctggga accacagcgc cttctggggc atgaccctgg atgaggccat 600
 tcgctaccgc ctgggcacca tccgcaccc ttcctcggtc atgaacatgc atgaaatatta 660
 tacagtgctg aaccaggggg aggtgcttcc cacagccttc gagggccttg agaagtggcc 720
 caacctgatt catgagccctc ttgaccaagg caactgtca ggctcctggg ccttctccac 780
 agcagctgtg gcatccgatc gtgtctcaat ccattctctg ggacacatga cgcctgttcc 840
 gtcgcggccag aacctgctgtt ctgtgacac ccaccagcag cagggctgccc ggggtggcg 900
 tctcgatggt gcctgggtt tctgcgtcg ccgagggggtg gtgtctgacc actgtaccc 960
 cttctcgggc cgtgaacgag acgaggctgg ccctgcggcc ccctgttatga tgcacagccg 1020
 agccatgggtt cggggcaagc ggcaggccac tgcccactgc cccaaacagct atgttaataa 1080
 caatgacatc taccagggtca ctcctgtcta ccgcctcgcc tccaaacgaca aggagatcat 1140
 gaaggagctg atggagaatg gcccgttca agccctcatg gaggtgcatg aggacttctt 1200
 cctataacaag ggaggcatct acagccacac gccagtggac cttggggaggc cagagagata 1260
 ccgcggccat gggacccact cagtcaagat cacaggatgg ggagaggaga cgctgccaga 1320

tggaaggacg ctcaaatact ggactgcggc caactcctgg ggcccagcct gggcgagag 1380
 gggccacttc cgcacatgtgc gcggcgtaa ttagtgcac atcgagagct tcgtgctggg 1440
 cgtctgggc cgcgtggca tggaggacat gggcatcac ttaggctgcg ggcaccacgc 1500
 ggggtccggc ctgggatcca ggctaaggc cggcgaaaga ggcccaatg gggcggtgac 1560
 cccagcctcg cccgacagag cccggggcgc aggccccgcg cagggcgcta atccccggcgc 1620
 gggttccgct gacgcagcgc cccgcctggg agccgcgggc aggcgagact ggcggagccc 1680
 ccagacctcc cagtggggac gggcaggc ctggcctggg aagagcacag ctgcagatcc 1740
 caggccctcg gcgcacccac tcaagactac caaagccagg acacctcaag tctccagccc 1800
 caataccccca ccccaatccc gtattttttt tttttttttt tttagacaggg tcttgctccg 1860
 ttgcccagggt tggagtgcag tggcccatca gggctcactg taacctccga ctccctgggtt 1920
 caagtgaccc tcccacctca gcctctcaag tagctggac tacaggtgca ccaccacacc 1980
 tggctaattt ttgtatTTTT tgtaaagagg ggggtctcac tgtgttgccc aggctggtt 2040
 cgaactcctg ggctcaagcg gtccacctgc ctccgcctcc caaagtgcgtg ggattgcagg 2100
 catgagccac tgcacccagc cctgtattct tattcttag atatttattt ttctttcac 2160
 tgttttaaaa taaaacccaaa gtattgataa aaaaaaaaaa 2197

<210> 12

<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

Met	Trp	Arg	Cys	Pro	Leu	Gly	Leu	Leu	Leu	Leu	Pro	Leu	Ala	Gly
1				5							10			15

His	Leu	Ala	Leu	Gly	Ala	Gln	Gln	Gly	Arg	Gly	Arg	Arg	Glu	Leu	Ala
						20			25				30		

Pro	Gly	Leu	His	Leu	Arg	Gly	Ile	Arg	Asp	Ala	Gly	Gly	Arg	Tyr	Cys
							35		40				45		

Gln	Glu	Gln	Asp	Leu	Cys	Cys	Arg	Gly	Arg	Ala	Asp	Asp	Cys	Ala	Leu
						50			55				60		

Pro	Tyr	Leu	Gly	Ala	Ile	Cys	Tyr	Cys	Asp	Leu	Phe	Cys	Asn	Arg	Thr
							65		70			75			80

Val	Ser	Asp	Cys	Cys	Pro	Asp	Phe	Trp	Asp	Phe	Cys	Leu	Gly	Val	Pro
									85				90		95

Pro	Pro	Phe	Pro	Pro	Ile	Gln	Gly	Cys	Met	His	Gly	Gly	Arg	Ile	Tyr
								100			105			110	

Pro	Val	Leu	Gly	Thr	Tyr	Trp	Asp	Asn	Cys	Asn	Arg	Cys	Thr	Cys	Gln
									115			120			125

Glu	Asn	Arg	Gln	Trp	His	Gly	Gly	Ser	Arg	His	Asp	Gln	Ser	His	Gln
								130			135			140	

Pro	Gly	Gln	Leu	Trp	Leu	Ala	Gly	Trp	Glu	Pro	Gln	Arg	Leu	Leu	Gly
								145			150			155	

His	Asp	Pro	Gly
-----	-----	-----	-----

<210> 13
 <211> 533
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (33)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (80)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (94)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (144)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (188)
 <223> a, t, c or g

<400> 13
 aggctcccttgc ccccttttc cacagcaagg ttntgcnatc ccgattcggt gtctcaaatc 60
 caattctctt gggacacatn acgcctgtcc ttngccccaa gaacctgttg tcttgtacac 120
 ccaccagcag cagggctgcc gcgntggcg tctcgatggt gcctgggtgg tccctgcgtcg 180
 ccgagggnntg gtgtctgacc actgctaccc cttctcgggc cgtgaacgag acgaggctgg 240
 ccctgcgc(cc ccctgtatga tgcacagccg agccatgggt cggggcaagc gccaggcac 300
 tgcccactgc cccaacagct atgttaataa caatgacatc taccaggtca ctcctgtcta 360
 ccgcctcggtc tccaacgaca aggagatcat gaaggagctg atggagaatg gcccgttcca 420
 agccctcatg gaggtgcattt aggacttctt cctataacaag ggaggcatct acagccacac 480
 gccagtgagc cttggggaggc cagagagata ccggccggcat gggaccact cag 533

<210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 14

<pre> ttcaggccct ctgagaagtgcgcc <210> 15 <211> 22 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe </pre> <pre> <400> 15 ggcggtatct ctctggcctc cc <210> 16 <211> 50 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe </pre> <pre> <400> 16 ttctcacacag cagctgtggc atccgatcgt gtctcaatcc attctctggg <210> 17 <211> 960 <212> DNA <213> Homo sapiens <400> 17 gtgtttgcc ctgttcatgg caggcttggc cctgcagcca ggcactgccc tgctgtgcta 60 ctcctgaaaa gcccagggtga gcaacgagga ctgcctgcag gtggagaact gcacccagct 120 gggggagcag tgctggaccg cgccatcccg cgcagttggc ctccctgaccg tcatcagcaa 180 aggctgcagc ttgaactcgt tggatgactc acaggactac tacgtggca agaagaacat 240 cacgtgtgt gacaccgact tgtgcaacgc cagccccccc catgcctgc agccggctgc 300 cgccatcctt ggcgtgttcc ctgcactcgg cctgctgttc tggggaccccg gccagctata 360 ggctctgggg ggcccccgctg cagccccacac tgggtgttgtt gccccaggcc tctgtgcac 420 tcctcacaga cctggcccaag tgggagcctg tcctggttcc tgaggcacat cctaacgcaa 480 gtctgaccat gtatgtctgc accccctgtcc cccaccctga ccctccatg gccccttc 540 ggactccac ccggcagatc agctctagtg acacagatcc gcctgcagat ggcccccttc 600 accctctctg ctgctgtttc catggcccag cattctccac ccttaaccct gtgctcaggc 660 acctttcccc ccaggaaggcc ttccctgccc accccatcta tgacttgagc caggtcttgt 720 ccgtgggtgc ccccgacacc agcaggggac aggcaactcag gagggcccag taaaggctga 780 gatgaagtgg actgagtaga actggaggac aagagtcgac gtgagttcct gggagtcctc 840 agagatgggg cctggaggcc tggaggaagg ggcaggcct cacatcgtg gggctccctg 900 aatggcagcc tgagcacagc tgaggccctt aataaacacc tgttggataa gccaaaaaaa 960 </pre> <pre> <210> 18 <211> 189 <212> PRT <213> Homo sapiens </pre>	24 22 50
---	------------------------

<400> 18
 Met Thr His Arg Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val
 1 5 10 15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu
 20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
 180 185

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 19

tgctgtgcta ctcctgcaaa gccc

24

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 20
tgcacaagtc ggtgtcacag cacg 24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 21
agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg 44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22
ccccacgcgtc cgaacctctc cagcgatggg agccgcgcgc ctgctgccca acctcactct 60
gtgcttacag ctgctgattc tctgtgtca aactcagtac gtgagggacc agggcgccat 120
gaccgaccag ctgagccaggc ggcagatccg cgagtaccaa ctctacagca ggaccagtgg 180
caagcacgtg caggtcacccg ggcgtcgcat ctccgcccacc gccgaggacg gcaacaagtt 240
tgccaagctc atagtggaga cggacacgtt tggcagccgg gttcgcatca aaggggctga 300
gagtggagaag tacatctgtt tgaacaagag gggcaagctc atcggaaagc ccagcgggaa 360
gagcaaaagac tgcgtgttca cggagatcgt gctggagaac aactatacgg cttccagaa 420
cgcccccac gagggtcttgt tcatggcctt cacgcggcag gggccggcccc gccaggcttc 480
ccgcagccgc cagaaccagc gcgaggccca cttcatcaag cgcctctacc aaggccagct 540
gccctcccc accacgcgg agaagcagaa gcagttcgag ttttgtggct ccccccac 600
ccgcccggacc aagcgcacac ggcggcccca gcccctcagc tagtctggga ggcaggggc 660
agcagccccct gggccgcctc cccacccctt tcccttctta atccaaggac tgggctgggg 720
tggcggagg ggagccagat ccccgaggga ggaccctcgag ggccgcgaag catccgagcc 780
cccagctggg aaggggcagg ccggtgcggc agggggcggt ggcacagtgc ccccttcccg 840
gacgggtggc aggcccttga gaggaaactga gtgtcaccct gatctcaggc caccagcctc 900
tgccggcctc ccagccggc tcctgaagcc cgctgaaagg tcagcgactg aaggccttgc 960
agacaaccgt ctggaggtgg ctgttctcaa aatctgcttc tcggatctcc ctcagtctgc 1020
ccccagcccc caaactcctc ctggctagac tgttaggaagg gacttttgg tgggggggg 1080
tttcaggaaa aaagaaaaggg agagagagga aaatagaggg ttgtccactc ctcacatcc 1140
acgaccagg cctgcacccc acccccaact cccagccccc gaataaaacc atttcctgc 1200

<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

<400> 23
 Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu
 1 5 10 15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr
 195 200 205

<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 24

cagtacgtga gggaccaggg cgccatga

28

<210> 25

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 25
 ccggtgacct gcacgtgctt gccca

24

<210> 26
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<220>
 <221> modified_base
 <222> (21)
 <223> a, t, c or g

<400> 26
 gcggatctgc cgcctgctca nctggtcggt catggcgccc t

41

<210> 27
 <211> 2479
 <212> DNA
 <213> Homo sapiens

<400> 27
 acttgcacatc acctgttgc agtgtggaaa aattctccct gttgaatttt ttgcacatgg 60
 aggacagcag caaagagggc aacacaggct gataagacca gagacagcag ggagattatt 120
 ttaccatacg ccctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180
 tccagtcat t tgat tttgc tg tttat tttt tttt ttttcc caccacattg 240
 t a t t t t a t t c c g t a c t t c a g a a t t g g g c c tacagaccac aaagtggccc agccatgggg 300
 c t t t t t c t t g a a g t c t t g g c t t a t t c a t t c c t g g g c t c t a c a g g t c a c a g g t c a c a g 360
 t c t g g c t g c c t a g t g t g t g c a c a g g a a c t t g t c t a c t g t a a t g a g c g a a 420
 g c t t g a c c t c a g t g c c t t g g g a t t c c g g a g g g c g t a a c c t g a c t c t a c c t c a c a a c a 480
 a c c a a t t a a t a t g c t g a t t c c t g c a g a a c t g c a c a a a t g a c t g c g t g c a c a c g g 540
 t c t a c t g t a t g c a a c t g a c g a a t t c a t t c c t t c a t t g g g c a a g a t t g c a g a g 600
 t t c t c c a t t t g c a g g a a a a c a a t t c a g a c a t t c c a t t g g g c t t g c c a g c t c t 660
 t g a a g c t t g a a g a g c t g c a c t g g a t g a c a t t c a c a g t g g g g g t g g a a g a c g 720
 g g g c t t c c g g a g g g c t a g c c t c a a a t t g t g t t t t g t c t a a g a a t t c a c t g a g c a 780
 g t g t g c t g t t g g g c t t c c t g a c t t g a g a g g c t g a g a t g g g a t g a a t t g c a 840
 c t g t c a t a t c c g a c a t g g g c t t c c a g a a t t c a g a c t t g g g c t t g g a g c g 900
 g g a a c c t c c t g a c c a a c a g g t a t c g c c g a g g g c a c t t c a c g c c a t c t c a c c a a g g c t c a 960
 a g g a a t t t c a a t t g t a c g t a a t t c g c t g t c c c a c c t c c t c a c c a g g c t c a 1020
 a t c t g a t c a g g c t c a t t t g c a g g a c a c c a g a t a a a c c a c a t t c t t g a c a g c t c t 1080
 c a a t c t g c g t a a g c t g g a a c g g c t g g a t a t c c a a c a a c c a a c t g c g g a t g c t a c t c 1140

aagggggtttt	tgataatctc	tccaacctga	agcagctac	tgctcgaa	aacccttgg	1200
tttgtgactg	cagtattaaa	tgggtcacag	aatggctcaa	atatatccct	tcatctctca	1260
acgtgcgggg	tttcatgtgc	caaggtctg	aacaagtccg	ggggatggcc	gtcaggaa	1320
taaatatgaa	tctttgtcc	tgtcccacca	cgacccccgg	cctgcctetc	ttcacccag	1380
cccccaagtac	agcttctccg	accactcagc	ctccccaccct	ctctattcca	aaccctagca	1440
gaagctacac	gcctccaact	cctaccacat	cgaaacttcc	cacgattct	gactggatg	1500
gcagagaaaag	agtgacccc	cctatttctg	aacggatcca	gctctctatc	cattttgtga	1560
atgataacttc	cattcaagtc	agctggctct	ctctcttcac	cgtatggca	tacaaactca	1620
catgggtgaa	aatgggccac	agtttagtag	ggggcatcg	tcaggagcgc	atagtcagcg	1680
gtgagaagca	acacctgagc	ctggtaact	tagagcccc	atccacctat	cggattttgt	1740
tagtgcacact	ggatgctttt	aactaccgcg	cggtagaaga	caccatttg	ttagaggcca	1800
ccacccatgc	ctccttatctg	aacaacggca	gcaacacagc	gtccagccat	gagcagacga	1860
cgtcccacag	catgggctcc	ccctttctgc	tggcgggctt	gatcgggggc	gcggtgat	1920
tttgtctggt	ggttttgctc	agcgttttt	gctggcatat	gcacaaaaag	ggcgctaca	1980
cctcccagaa	gtggaaatac	aaccggggcc	ggcggaaaga	tgattattgc	gaggcaggca	2040
ccaagaagga	caactccatc	ctggagatga	cagaaaccag	ttttagatc	gtctccctaa	2100
ataacgatca	actccttaaa	ggagattca	gactgcagcc	catttacacc	ccaaatgggg	2160
gcattaatta	cacagactgc	catatcccc	acaacatgcg	atactgcaac	agcagcgtgc	2220
cagacctgga	gcactgccc	acgtgacagc	cagaggccca	gcgttatcaa	ggcggacaat	2280
tagactctt	agaacacact	cgtgtgtca	cataaagaca	cgcagattac	atttgataaa	2340
tgttacacag	atgcatttgc	gcatttgaat	actctgtat	ttatacggtg	tactatataa	2400
tgggatttaa	aaaaagtgc	atctttcta	tttcaagtt	attacaaaca	gttttgcata	2460
tctttgtttt	ttaaatctt					2479

<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu

1 5 10

15

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
 20 25 30

20 25 30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
 35 40 45

35 40 45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
50 55 60

50 55 60

Val	Thr	Val	Leu	Tyr	Leu	His	Asn	Asn	Gln	Ile	Asn	Asn	Ala	Gly	Phe
65				70						75					80

65 70 75

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
85 90 95

85 90

95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
100 105 110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
115 120 125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser
 130 135 140
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser
 145 150 155 160
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
 165 170 175
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile
 180 185 190
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg
 195 200 205
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly
 210 215 220
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
 225 230 235 240
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
 245 250 255
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe
 260 265 270
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu
 275 280 285
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln
 290 295 300
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp
 305 310 315 320
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly
 325 330 335
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu
 340 345 350
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro
 355 360 365
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro
 370 375 380
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro
 385 390 395 400
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

405	410	415	
Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val			
420	425	430	
Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met			
435	440	445	
Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly			
450	455	460	
Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu			
465	470	475	480
Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu			
485	490	495	
Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala			
500	505	510	
Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser			
515	520	525	
His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala			
530	535	540	
Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser			
545	550	555	560
Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys			
565	570	575	
Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly			
580	585	590	
Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln			
595	600	605	
Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu			
610	615	620	
Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His			
625	630	635	640
Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu			
645	650	655	
His Cys His Thr			
660			
<210> 29			
<211> 21			
<212> DNA			

<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 29
cggctcaccc gtatggcaac c

21

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 30
gcaggacaac cagataaaacc ac

22

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 31
acgcagattt gagaaggctg tc

22

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 32
ttcacgggct gctcttgccc agctttgaa gcttgaagag ctgcac

46

<210> 33
<211> 3449
<212> DNA
<213> Homo sapiens

<400> 33
acttggagca agcggcgccg gcggagacag aggcagaggc agaagctggg gctccgtcct 60
cgcctccac gagcgatccc cgaggagagc cgcggccctc ggcgaggcga agaggccgac 120

ctgtagaaca ctggccatag gaaatgctgt tttttgtac tggactttac cttgatata 3360
 gtatatggat gtatgcataa aatcatagga catatgtact tgtggaacaa gttggattt 3420
 ttatacataa ttaaaaattca ccacttcag 3449

<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile
 1 5 10 15

Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
 20 25 30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
 35 40 45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
 50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
 65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
 85 90 95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
 100 105 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
 115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
 130 135 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
 145 150 155 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
 165 170 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
 180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
 195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
 210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

225	230	235	240
Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile			
245	250	255	
Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser			
260	265	270	
Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His			
275	280	285	
Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln			
290	295	300	
Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala			
305	310	315	320
Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val			
325	330	335	
Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu			
340	345	350	
Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn			
355	360	365	
Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr			
370	375	380	
Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys			
385	390	395	400
Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu			
405	410	415	
Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe			
420	425	430	
Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu			
435	440	445	
Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser			
450	455	460	
Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys			
465	470	475	480
Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu			
485	490	495	
His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu			
500	505	510	

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val
 515 520 525
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp
 530 535 540
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp
 545 550 555 560
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly
 565 570 575
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys
 580 585 590
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys
 595 600 605
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser
 610 615 620
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile
 625 630 635 640
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu
 645 650 655
 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn
 660 665 670
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly
 675 680 685
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser
 690 695 700
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
 705 710 715 720
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
 725 730 735
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
 740 745 750
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
 755 760 765
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
 770 775 780
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln
 805 810 815
 Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu
 820 825 830
 Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp
 835 840 845
 Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser
 850 855 860
 Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu
 865 870 875 880
 Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln
 885 890 895
 Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu
 900 905 910
 Arg Tyr Arg
 915

<210> 35
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 35
 gtgaccctgg ttgtgaatac tcc

23

<210> 36
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 36
 acagccatgg tctatagctt gg

22

<210> 37
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 37
 gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag 45
 <210> 38
 <211> 1813
 <212> DNA
 <213> Homo sapiens
 <400> 38
 ggagccgccc tgggtgtcag cggctcggt cccgcgcacg ctccggccgt cgccgcaggct 60
 cggcacctgc aggtccgtgc gtccccggc tggcccccgt gactccgtcc cggccaggaa 120
 gggccatgtat ttccctcccg gggcccccgg tgaccaactt gctgcgggtt ttgttcctgg 180
 ggctgagtgc ctcgcgcgc ccctcgccgg cccagctgca actgcacttg cccgccaacc 240
 ggttgcaggc ggtggaggga ggggaagtgg tgcttccagc gtggtaacacc ttgcacgggg 300
 aggtgttttc atcccagcca tgggagggtgc ccttgcgtat gtggtttttc aaacagaaaag 360
 aaaaggagga tcaggtgttg tcctacatca atgggtcac aacaagcaaa cctggagttat 420
 ctttgtcta ctccatgcgc tcccgaaacc tgcgtccgtcg gctggagggt ctccaggaga 480
 aagactctgg cccctacagc tgctccgtga atgtcaaga caaacaaggc aaatcttaggg 540
 gccacagcat caaaacctta gaactcaatg tactggttcc tccagctctt ccattctgcc 600
 gtctccagggt tggcccccgt gtgggggcaaa acgtgacccct gagctgccag tctccaagga 660
 gtaagccgc tggccaaatac cagtgggatc ggcagcttcc atccctccag actttcttg 720
 caccaggatt agatgtcatc cgtgggtctt taaggctcactt caacccctcg tcttccatgg 780
 ctggagtcta tggctgcgaag gcccacaatg aggtgggacac tgcccaatgt aatgtgacgc 840
 tggaaagttag cacaggccct ggagctgcag tgggtgttgg agctgttgg ggtacccctgg 900
 ttggactggg gttgtggct gggctggcc tcttgcacca ccgcggggc aaggccctgg 960
 aggagccagc caatgatatac aaggaggatg ccattgcctt ccggacccctg ccctggccca 1020
 agagctcaga cacaatctcc aagaatgggaa cccttccttc tgtcacctcc gcacgagccc 1080
 tccggccacc ccatggccctt cccaggccctg gtgcatttgcac ccccaacggcc agtctctcca 1140
 gccaggccctt gcccctacca agactgcccac ccacagatgg ggcccacccctt caaccaatata 1200
 ccccccattttt tgggtgggggtt tcttcccttg gcttgcacccatgggtgtt gtgcctgtga 1260
 tgggtgcctgc ccagagtcaa gctggctctc tggatgtatg accccaccac tcattggctt 1320
 aaggattttgg ggtctctctt tcctataagg gtcaccccttca gcacagaggc ctgagtcatg 1380
 ggaaagagtc acactccttgc cccttagtac tctgccccca cctctcttta ctgtggggaaa 1440
 accatctcag taagacctaa gtgtccagga gacagaagga gaagaggaag tggatctgga 1500
 attggagga gcctccaccc accccctgact cctcccttatg aagccagctg ctgaaatatt 1560
 ctactcacca agagtgggg gcagagactt ccagtcaactg agtctccctg gcccccttga 1620
 tctgtacccc accccctatctt aacaccaccc ttggctccca ctccagctcc ctgtatttggat 1680
 ataacactgtc aggctggctt ggttaggtt tactggggca gaggataggg aatctttat 1740
 taaaactaac atgaaatatacg tggatgttttcaatttgcattttaaaataaag atacataatg 1800
 tttgtatgaa aaa 1813
 <210> 39
 <211> 390
 <212> PRT
 <213> Homo sapiens
 <400> 39
 Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1	5	10	15
Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln			
20	25	30	
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val			
35	40	45	
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln			
50	55	60	
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys			
65	70	75	80
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro			
85	90	95	
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg			
100	105	110	
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val			
115	120	125	
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr			
130	135	140	
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu			
145	150	155	160
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser			
165	170	175	
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro			
180	185	190	
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser			
195	200	205	
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys			
210	215	220	
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu			
225	230	235	240
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly			
245	250	255	
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His			
260	265	270	
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp			
275	280	285	

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
370 375 380

Gln Ala Gly Ser Leu Val
385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> De

oligonucleotide probe

agggtctc

—
—
—
—
—

22

<211> 24

<212> DN

<213> Art

<223>

oligonucleotide probe

attgtggaa

115-55511-112-0000000000

24

<211> 50

<212> DN

<213> Art.

223

oligonucleotide probe

<400> 42		
ggccacagca tcaaaacctt agaactcaat gtactggtc ctccagctcc		50
<210> 43		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 43		
gtgtgacaca gcgtggc		18
<210> 44		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 44		
gaccggcagg cttctgcg		18
<210> 45		
<211> 25		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 45		
cagcagcttc agccaccagg agtgg		25
<210> 46		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 46		
ctgagccgtg ggctgcagtc tcgc		24
<210> 47		

tgtataaaaa	tgactcatca	aattatccaa	ttattaacta	ctagacaaaa	agtattttaa	2220
atcagttttt	ctgttatgc	tataggaact	gtagataata	aggtaaaatt	atgtatcata	2280
tagatatact	atgttttct	atgtgaaata	gttctgtcaa	aatagtatt	gcagatattt	2340
ggaaaagtaat	tggtttctca	ggagtgatat	cactgcaccc	aaggaaagat	tttctttcta	2400
acacgagaag	tatataatgc	tcctgaagga	aaccactggc	ttgatatttc	tgtgactcgt	2460
gttgcctttg	aaactagtcc	cctaccacct	cggtaatgag	ctccattaca	gaaagtggaa	2520
cataagagaa	tgaaggggca	gaatatcaaa	cagtgaaaag	ggaatgataa	gatgtatttt	2580
gaatgaactg	tttttctgt	agactagctg	agaaaatttgt	gacataaaat	aaagaattga	2640
agaaaacacat	tttaccattt	tgtgaattgt	tctgaactta	aatgtccact	aaaacaacct	2700
agacttctgt	ttgctaaatc	tgtttctttt	tctaataattc	aaaaaaaaaa	aaaaagggtt	2760
acctccacaa	attgaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	2820
aa						2822

<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
20 25 30

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
 35 40 45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
50 55 60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
65 70 75 80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
85 90 95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
100 105 110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
115 120 125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
 130 135 140

Glu	Val	Tyr	Arg	Asn	Ser	Val	Thr	Asp	Leu	Ser	Pro	Thr	Asp	Ile	Ile
145					150					155					160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
165 170 175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

180	185	190
Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val		
195	200	205
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys		
210	215	220
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe		
225	230	235
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys		
245	250	255
Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met		
260	265	270
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala		
275	280	285
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser		
290	295	300
Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln		
305	310	315
Asn Tyr Asp Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile		
325	330	335
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys		
340	345	350
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser		
355	360	365
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp		
370	375	380
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser		
385	390	395
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly		
405	410	415
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln		
420	425	430
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr		
435	440	445
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys		
450	455	460

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
 465 470 475 480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
 485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
 500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
 515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
 530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
 545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
 565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
 580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
 595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
 610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
 625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
 645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
 660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
 675 680 685

Leu Arg
 690

<210> 50
 <211> 589
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (61)

<223> a, t, c or g

<400> 50

tggaaaacata tcctccctca tatgaatatg gatggagact acataaatat atttccaaag 60
 ngaaaagccg gcatatggat tcaaattggca atgttgcagt tgcatttttta tattataaga 120
 gtatttgtcc ctttgcttc atcatctgac aacttcttat tgaaacctca aaattatgat 180
 aattctgaag aggagggaaag agtcataatct tcagtaattt cagtcataat gagctcaa 240
 ccaccacat tatatgaact tgaaaaaaata acatttacat taagtcatacg aaaggcaca 300
 gataggtata ggagtctatg tggcattttg gaataactcac ctgataccat gaatggcagc 360
 tggcttcag agggctgtga gctgacatac tcaaattgaga cccacacccat atgccgtgt 420
 aatcacctga cacatttgc aattttgatg tcctctggc cttccattgg tattaaagat 480
 tataatattc ttacaaggat cactcaacta ggaataatta tttcactgat ttgtcttgcc 540
 atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 52

ggagtagaaaa gcgcattgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 53

cacctgataac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 54
cgagctcgaa ttaattcg 18

<210> 55
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 55
ggatccctg agtcagg 18

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 56
cctagtttag tgatccttgt aag 23

<210> 57
<211> 50
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 57
atgagaccca cacctcatgc cgctgtataatc acctgacaca ttttgcaatt 50

<210> 58
<211> 2137
<212> DNA
<213> Homo sapiens

<400> 58
gctcccgcc aagaacctcg gggccgctgc gcgggtgggga ggagttcccc gaaaccggc 60
cgctaagcga ggcctccccc tcccgagat ccgaacggcc tggggcgggt caccggct 120

gggacaagaa gccgcgcct gcctgccccg gccccgggag ggggctgggg ctggggccgg 180
 aggccgggtg tgagtgggtg tgtgcggggg gccggaggctt gatcaatcc cgataagaaa 240
 tgctcgggtg tcttgggcac ctaccctgtgg gccccgttaag gcgctactat ataaggctgc 300
 cggcccccggag ccggccgcgc gtcagagcag gagcgctgcg tccaggatct agggccacga 360
 ccatccaaac ccggcactca cagccccgca ggcgcattccg gtcggccgcggc agcctccgc 420
 acccccatacg ccggagactgc gccgagagcc ccaggaggt gccatgcgga gccccgtgt 480
 ggtggtccac gtatggatcc tggccggcct ctggctggcc gtggccggc gccccctcgc 540
 cttctcgac gcggggcccc acgtgcacta cggctggggc gaccctatcc gcctgcggca 600
 cctgtacacc tccggcccc acgggcttc cagctgcctc ctgcgcattcc gtggccacgg 660
 cgtcggtggac tgcgccggg gccagagcgc gcacagttt ctggagatca aggcaactgc 720
 tctgcggacc gtggccatca agggcgtgca cagcgtgcgg tacctctgca tgggcgcgca 780
 cggcaagatg caggggctgc ttcaacttc gggagaagac tgtgtttcg aggaggagat 840
 ccccccagat ggctacaatg tgtaccgatc cgagaagcac cgcctcccg tctccctgag 900
 cagtgccaaa cagcggcagc tgtacaagaa cagaggctt cttcaactct ctcatttcct 960
 gcccatgctg cccatggtcc cagaggagcc tgaggacotc agggccact tggaaatctga 1020
 catgttctct tcgccccctgg agaccgacag catggaccga tttgggcttg tcaccggact 1080
 ggaggccgtg aggagtccca gctttgagaa gtaactgaga ccatggccgg gcctttcac 1140
 tgctgccagg ggctgtggta cctgcagcgt gggggacgtg cttctacaag aacagtctg 1200
 agtccacgtt ctgttttagct ttaggaagaa acatctagaa gttgtacata ttcaagat 1260
 tccattggca gtgccagtt ctggcaata gacttgtctg atcataacat tgtaagctg 1320
 tagctgccc agctgctgcc tggggcccca ttctgctccc tcgaggttgc tggacaagct 1380
 gctgcaactgt ctcaacttctg cttgaataacc tccatcgatg gggactcac ttcccttgga 1440
 aaaattctta tgtcaagctg aaattctcta atttttctc atcaattccc caggagcagc 1500
 cagaagacag gcagtagtt taatttcagg aacaggtgat ccactctgta aaacagcagg 1560
 taaatttcac tcaacccat gtgggaattt atctataatct ctacttccag ggaccatgg 1620
 cccttcccaa atccctccag gccagaactg actggagcag gcatggccca ccaggcttca 1680
 ggagtagggg aagcctggag ccccaactcca gcccctggac aacttgagaa ttccccctga 1740
 ggccagttct gtcatggatg ctgtcctgag aataacttgc tgtcccggtg tcacctgttt 1800
 ccatctccca gcccaccagc cctctgccc ctcacatgc ctcccatgg attggggcct 1860
 cccagcccccc ccaccttatg tcaacctgca ctcttgc 15 1920
 atttgaagac ccaagtctt gtcaataact tgctgtgtgg aagcagcggg ggaagaccta 1980
 gaacccttccca cccagcactt ggtttccaa catgatattt atgagtaatt tattttgata 2040
 tgtacatctc ttatttctt acattattta tgcccccaaa ttatattat gtatgtaaat 2100
 gaggtttgtt ttgtatattta aaatggagtt tgtttgt 2137

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

Met	Arg	Ser	Gly	Cys	Val	Val	Val	His	Val	Trp	Ile	Leu	Ala	Gly	Leu
1					5			10			15				

Trp	Leu	Ala	Val	Ala	Gly	Arg	Pro	Leu	Ala	Phe	Ser	Asp	Ala	Gly	Pro
			20					25			30				

His	Val	His	Tyr	Gly	Trp	Gly	Asp	Pro	Ile	Arg	Leu	Arg	His	Leu	Tyr
									35			40		45	

Thr	Ser	Gly	Pro	His	Gly	Leu	Ser	Ser	Cys	Phe	Leu	Arg	Ile	Arg	Ala
									50			55		60	

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
 65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
 85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
 100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
 115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
 130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
 145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
 165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
 180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
 195 200 205

Val Arg Ser Pro Ser Phe Glu Lys
 210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 60

atccggccag atggctacaa tgtgtta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 61

gcctccccgt ctcccctgagc agtgccaaac agcggcagtg ta

42

<210> 62
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 62
ccagtcgggt gacaagccca aa 22

<210> 63
<211> 1295
<212> DNA
<213> Homo sapiens

<400> 63
cccagaagtt caagggcccc cggcctcctg cgctcctgcc gccgggaccc tcgacccct 60
cagagcagcc gcgtgcgcgc ccgggaagat ggcgaggagg agccgcacc gcctccct 120
gctgctgctg cgctacctgg tggtcgcctt gggctatcat aaggcctatg gttttctgc 180
cccaaaagac caacaagtag tcacacgact agagtaccaa gaggctattt tagcctgaa 240
aaccccaag aagactgtt cctccagatt agagtggaaag aaactggtc ggagtgtctc 300
ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360
tttcaataatc cggatcaaaa atgtgacaag aagtgtatgcg gggaaatatc gttgtgaagt 420
tagtgcccca tctgagcaag gccaaaacctt ggaagaggat acagtcactc tggaaagtatt 480
agtggctcca gcagttccat catgtgaagt accctcttct gctctgagtg gaactgtgg 540
agagctacga tgtcaagaca aagaaggaa tccagctcct gaatacacat gtttaagga 600
tggcatccgt ttgctagaaa atcccagact tggctccaa agcaccaaca gctcatacac 660
aatgaataaca aaaactggaa ctctgcaatt taatactgtt tccaaactgg acactggaga 720
atattccctgt gaagccccca attctgttgg atatcgagg tgcctggaa aacgaatgca 780
agtagatgat ctcaacataa gtggcatcat agcagccgta gtgttgtgg ctttagtgat 840
ttccgttgtt ggcctgggt tatgctatgc tcagaggaaa ggctacttt caaaaagaaac 900
ctccttccag aagagtaatt cttcatctaa agccacgaca atgagtgaaa atgtgcagtg 960
gctcacgcct gtaatcccgactttggaa ggcgcggcg ggcggatcac gaggtcagga 1020
gttctagacc agtctggcca atatggtaa accccatctc tactaaaata caaaaattag 1080
ctggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140
acccggggagg cggaggttgc agtgagctga gatcacgcca ctgcagttca gcctggtaa 1200
cagagcaaga ttccatctca aaaaataaaaa taaataaaata aataaataact gtttttacc 1260
tgtagaattc ttacaataaa tatacgcttga tattc 1295

<210> 64
<211> 312
<212> PRT
<213> Homo sapiens

<400> 64
Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr
1 5 10 15

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
 35 40 45

Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
 50 55 60

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
 65 70 75 80

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
 85 90 95

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
 100 105 110

Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
 115 120 125

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
 130 135 140

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
 145 150 155 160

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
 165 170 175

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
 180 185 190

Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp
 195 200 205

Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg
 210 215 220

Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
 225 230 235 240

Ile Ala Ala Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu
 245 250 255

Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser
 260 265 270

Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn
 275 280 285

Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala
 290 295 300

Gly Gly Ser Arg Gly Gln Glu Phe

305

310

<210> 65
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 65
atcggtgtga agtttagtgcc cc

22

<210> 66
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 66
acctgcgata tccaacagaa ttg

23

<210> 67
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 67
ggaagaggat acagtcaactc tggaagtatt agtggctcca gcagttcc

48

<210> 68
<211> 2639
<212> DNA
<213> Homo sapiens

<400> 68
gacatcgag gtgggcttagc actgaaaactg cttttcaaga cgaggaagag gaggagaaaag 60
agaaaagaaga ggaagatgtt gggcaacatt tatttaacat gctccacagc ccggaccctg 120
gcatcatgct gctattcctg caaatactga agaagcatgg gatttaata ttttacttct 180
aaataaatga attactcaat ctccttatgac catctataca tactccacct tcaaaaagta 240
catcaatatt atatcattaa ggaaatagta accttctt ctccaatatg catgacattt 300
ttggacaatg caattgtggc actggcactt attcagtgta agaaaaactt tgtggttcta 360
tggcattcat catttgacaa atgcaagcat cttccttatac aatcagctcc tattgaactt 420
actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480
tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagta 540

aagctgtaga taaaaaaagtg gattgtccac ggttatgtac gtgtgaaaatc aggccttgg 600
 ttacacccag atccatttat atggaagcat ctacagtggta ttgtaatgtat ttaggtcttt 660
 taacttccc agccagattg ccagctaaca cacagattct tctctacag actaacaata 720
 ttgcaaaaat tgaataactcc acagacttcc cagtaaacct tactggcctg gatttatactc 780
 aaaacaattt atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctccttctg 840
 tgtacctaga gaaaaacaaa cttactgaac tgcctgaaaa atgtctgtcc gaactgagca 900
 acttacaaga actctataatt aatcacaact tgcttctac aatttcacct ggagccttta 960
 ttggcctaca taatottctt cgacttcatac tcaattcaaa tagattgcag atgatcaaca 1020
 gtaagtggtt ttagtgcctt ccaaatactag agattctgtat gattggggaa aatccaatta 1080
 tcagaatcaa agacatgaac tttaaggcctc ttatcaatct tcgcagcctg gttatagctg 1140
 gtataaacct cacagaaaata ccagataacg ccttggttgg actggaaaac ttagaaagca 1200
 tctctttta cgataacagg cttattaaag taccccatgt tgcttcaa aaagttgtaa 1260
 atctcaaattt tttggatcta aataaaaaatc ctattaatag aatacgaagg ggtgattta 1320
 gcaatatgtt acactttaaa gagttggggaa taaataatat gcctgagctg atttccatcg 1380
 atagtcttcg tggataaac ctgcagatt taagaaaaat agaagctact aacaacccta 1440
 gattgtctta cattcacccc aatgcatttt tcagactccc caagctggaa tcactcatgc 1500
 tgaacagcaa tgctctcagt gccctgtacc atggtaccat tgagtctctg ccaaacccta 1560
 agggaaatcag catacacagt aaccccatca ggtgtgactg tgcataccgt tggatgaaca 1620
 tgaacaaaac caacattcga ttcatggagc cagattcact gtttgcgtg gacccacctg 1680
 aattccaagg tcagaatgtt cggcaagtgc atttcagggaa catgtggaa atttgtctcc 1740
 ctcttatacg tcctgagagc ttcccttcta atctaaatgt agaagctggg agctatgttt 1800
 ccttcactg tagagctact gcagaaccac gcctgaaat ctactggata acaccccttg 1860
 gtcaaaaact cttgcctaatt accctgacag acaagttcta tgccattct gagggaaacac 1920
 tagatataaa tggcgtaact cccaaagaag ggggtttata tactgtata gcaactaacc 1980
 tagttggcgc tgacttgaag tctttatga tcaaagtggaa tggatcttt ccacaagata 2040
 acaatggcgc tttgaatatt aaaataagag atattcagggc caattcagtt ttgggtgcct 2100
 ggaaagcaag ttctaaaatt ctcaatcta gtgttaaatg gacagccctt gtcaagactg 2160
 aaaattctca tgctgcgcaa agtgcctgaa taccatctga tgtcaaggta tataatctta 2220
 ctcatctgaa tccatcaact gatataaaa tttgttattga tattccacc atctatcaga 2280
 aaaacagaaaaaaaatgtta aatgtcacca ccaaagggtt gcacccctgat caaaaagagt 2340
 atgaaaaagaa taataccaca acacttatgg cctgtcttgg aggccctctg gggattattg 2400
 gtgtgatatg tcttatcagc tgcctctctc cagaaatgaa ctgtgatggt ggacacagct 2460
 atgtgaggaa ttacttacag aaaccaacct ttgcatttagg tgagctttat cctcctctga 2520
 taaatctctg ggaagcagga aaagaaaaaa gtacatcaact gaaagtaaaa gcaactgtta 2580
 tagtttacc aacaaatatg tcctaaaaac caccaaggaa acctactcca aaaaatgaac 2639

<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

Met	Lys	Asp	Met	Pro	Leu	Arg	Ile	His	Val	Leu	Leu	Gly	Leu	Ala	Ile
1															15

Thr	Thr	Leu	Val	Gln	Ala	Val	Asp	Lys	Lys	Val	Asp	Cys	Pro	Arg	Leu
															30

Cys	Thr	Cys	Glu	Ile	Arg	Pro	Trp	Phe	Thr	Pro	Arg	Ser	Ile	Tyr	Met
															45

Glu	Ala	Ser	Thr	Val	Asp	Cys	Asn	Asp	Leu	Gly	Leu	Leu	Thr	Phe	Pro
															50

DRAFT VERSION 1.02

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Gln Thr Asn Asn
 65 70 75 80

Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly
 85 90 95

Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val
 100 105 110

Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu
 115 120 125

Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu
 130 135 140

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe
 145 150 155 160

Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu
 165 170 175

Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile
 180 185 190

Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe
 195 200 205

Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu
 210 215 220

Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
 225 230 235 240

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu
 245 250 255

Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile
 260 265 270

Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu
 275 280 285

Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala
 290 295 300

Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro
 305 310 315 320

Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu
 325 330 335

Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
405	410	415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
420	425	430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
435	440	445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
450	455	460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
465	470	475
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
485	490	495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
500	505	510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
515	520	525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
530	535	540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
545	550	555
560		
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
565	570	575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
580	585	590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
 675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
690 695 700

Thr Asn Met Ser
705

<210> 70
<211> 1305
<212> DNA
<213> *Homo sapiens*

<210> 71
<211> 259
<212> PRT
<213> *Homo sapiens*

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu
 1 5 10 15

Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser
 20 25 30

Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val
 35 40 45

Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro
 50 55 60

Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro
 65 70 75 80

Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser
 85 90 95

Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala
 100 105 110

Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val
 115 120 125

His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn
 130 135 140

Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met
 145 150 155 160

Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val
 165 170 175

Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala
 180 185 190

Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val
 195 200 205

Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr
 210 215 220

Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys
 225 230 235 240

Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser
 245 250 255

Thr Val Val

<210> 72
 <211> 2290

<212> DNA
<213> Homo sapiens

<400> 72
accgagccga gcggaccgaa ggcgccccc agatcaggt gagcaagagg atgctggcgg 60
ggggcgtag gacatgccc agccccctcc tggcctgctg gcagcccatc ctcctgctgg 120
tgctggctc agtgcgtca ggctcgcca cgggctgccc gccccgtgc gagtgctccg 180
cccaggaccg cgctgtgctg tgccaccgca agtgcgttgc ggcagtcggc gagggcatcc 240
ccaccgagac ggcgtgtcg gacctaggca agaaccgcata caaaacgcctc aaccaggacg 300
agttcgccag cttcccgac ctggaggagc tggagctcaa cgagaacatc gtgagcggcc 360
tggagccgg cgcctcaac aacctttca acctccggac gctgggtctc cgcagcaacc 420
gcctgaagct catcccgcta ggcgtttca ctggcctcag caactgtacc aagcaggaca 480
tcagcgagaa caagatcgat atcctactgg actacatgtt tcagcacgt tacaaccta 540
agtcaactgga gttggcgcac aatgacatcg tctacatctc tcacccgcgc tttagcgcc 600
tcaacagcc ggagcagctg acgctggaga aatgcaacatc gacccatc cccaccgagg 660
cgctgtccca cctgcacggc ctcatgtcc tgaggctccg gcacctcaac atcaatgcca 720
tccggacta ctccctcaag aggctgtacc gactcaaggt ctggagatc tcccactggc 780
cctacttggc caccatgaca cccaaactgccc tctacggcct caacctgacg tccctgttca 840
tcacacactg caatctgacc gctgtccct acctccggcgt ccgcacccata gtctatctcc 900
gcttcctcaa cctctccatc aaccccatca gcaccattga gggctccatg ttgcatgagc 960
tgctccggct gcaggagatc cagctggcgg gccccggcgt ggcgtggcgg gagccctatg 1020
ccttcggcgg cctcaactac ctgcgtgtc tcaatgtctc tggcaaccag ctgaccacac 1080
tggaggaatc agtctccac tcgggtggca acctggagac actcatctg gactccaacc 1140
cgctggctc cgactgtcgg ctccctgtgg tggccggcgg ccgtggcgg ctcaacttca 1200
accggcagca gcccacgtgc gccacccggc agtttgcata gggcaaggag ttcaaggact 1260
tccctgatgt gctactgccc aactacttca cctgcgcgcg cggccgcata cgggaccgca 1320
aggcccgca ggtgtttgtg gacgaggggcc acacgggtgc gtttgtgtgc cggggccatg 1380
gcgaccggcc gcccgcaccc ctctggctct caccggaaa gcacccgtgc tcagccaaga 1440
gcaatggcgg gtcacacgtc ttccctgatg gcacgtggc ggtggcgtac gcccaggatc 1500
aggacaacgg cacgtacctg tgcatcgccg ccaacggggcc cggcaacgc tccatgccc 1560
cccacctgca tggcgccgcg tactcgcccg actggccca tcagcccaac aagaccttcg 1620
cttcatctc caaccagccg ggccggggag aggccaaacag caccggcgc actgtgcctt 1680
tccccctcga catcaagacc ctcatcatcg ccaccacat gggcttcata tctttcttgg 1740
gcgtcgctct cttctgcctg gtgtgtgtt ttctctggag cggggggcaag ggcaacacaa 1800
agcacaacat cgagatcgag tatgtgcccc gaaagtccgcg cgcaggcatc agtccggcc 1860
acgcggccccc caagttcaac atgaagatga tatgaggccg gggccgggggg cagggacccc 1920
cgccggccgc ggcaggggaa gggccctggc cgcacccatc tcactctcca gtccttccca 1980
cctccctccct acccttctac acacgttctc tttctccctc ccgcctccgt cccctgtgc 2040
ccccggccag ccctcaccac ctgcctcct tctaccagga cctcagaagc ccagacccatgg 2100
ggacccacc tacacagggg cattgacaga ctggagttga aagccgacga accgacacgc 2160
ggcagagtca ataattcaat aaaaaagttt cgaactttct ctgttaacttg ggtttcaata 2220
attatggatt tttatgaaaa cttgaaataa taaaaagaga aaaaaactaa aaaaaaaaaa 2280
aaaaaaaaaa 2290

<210> 73
<211> 620
<212> PRT
<213> Homo sapiens

<400> 73
Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro
1 5 10 15

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly
 20 25 30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
 35 40 45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala
 50 55 60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
 65 70 75 80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
 85 90 95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro
 100 105 110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser
 115 120 125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn
 130 135 140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp
 145 150 155 160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp
 165 170 175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser
 180 185 190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
 195 200 205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His
 210 215 220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
 225 230 235 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr
 245 250 255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His
 260 265 270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr
 275 280 285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly
 290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly
 305 310 315 320

Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr
 325 330 335

Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu
 340 345 350

Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser
 355 360 365

Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg
 370 375 380

Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu
 385 390 395 400

Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro
 405 410 415

Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln
 420 425 430

Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala
 435 440 445

Asp Gly Asp Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His
 450 455 460

Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly
 465 470 475 480

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu
 485 490 495

Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu
 500 505 510

His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr
 515 520 525

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr
 530 535 540

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala
 545 550 555 560

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu
 565 570 575

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580	585	590
Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser		
595	600	605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile		
610	615	620

<210> 74

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 74

tcacacctggag ccttttattgg cc

22

<210> 75

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 75

ataccaggcta taaccaggct gcg

23

<210> 76

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 76

caacagtaag tggtttgatg ctcttccaaa tcttagagatt ctgatgatttg
gg

50

52

<210> 77

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 77 ccatgtgtct ctcctacaa ag	22
<210> 78 <211> 23 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 78 ggaaatagat gtgatctgat tgg	23
<210> 79 <211> 50 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 79 cacctgttagc aatgcaaatc tcaaggaaat acctagagat cttccctcctg	50
<210> 80 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 80 agcaaccgc tgaagctcat cc	22
<210> 81 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 81 aaggcgccgtt gaaagatgta gacg	24
<210> 82	

Met	Gly	Ala	Pro	Ala	Ala	Ser	Leu	Leu	Leu	Leu	Leu	Phe	Ala		
1						5							15		
Cys	Cys	Trp	Ala	Pro	Gly	Gly	Ala	Asn	Leu	Ser	Gln	Asp	Asp	Ser	Gln
					20				25				30		
Pro	Trp	Thr	Ser	Asp	Glu	Thr	Val	Val	Ala	Gly	Gly	Thr	Val	Val	Leu
						35		40					45		
Lys	Cys	Gln	Val	Lys	Asp	His	Glu	Asp	Ser	Ser	Leu	Gln	Trp	Ser	Asn
						50		55				60			
Pro	Ala	Gln	Gln	Thr	Leu	Tyr	Phe	Gly	Glu	Lys	Arg	Ala	Leu	Arg	Asp
					65		70			75				80	
Asn	Arg	Ile	Gln	Leu	Val	Thr	Ser	Thr	Pro	His	Glu	Leu	Ser	Ile	Ser
					85				90					95	
Ile	Ser	Asn	Val	Ala	Leu	Ala	Asp	Glu	Gly	Glu	Tyr	Thr	Cys	Ser	Ile
					100			105					110		
Phe	Thr	Met	Pro	Val	Arg	Thr	Ala	Lys	Ser	Leu	Val	Thr	Val	Leu	Gly
					115			120					125		
Ile	Pro	Gln	Lys	Pro	Ile	Ile	Thr	Gly	Tyr	Lys	Ser	Ser	Leu	Arg	Glu
					130		135				140				
Lys	Asp	Thr	Ala	Thr	Leu	Asn	Cys	Gln	Ser	Ser	Gly	Ser	Lys	Pro	Ala
					145		150			155				160	
Ala	Arg	Leu	Thr	Trp	Arg	Lys	Gly	Asp	Gln	Glu	Leu	His	Gly	Glu	Pro
					165				170				175		
Thr	Arg	Ile	Gln	Glu	Asp	Pro	Asn	Gly	Lys	Thr	Phe	Thr	Val	Ser	Ser
					180			185					190		
Ser	Val	Thr	Phe	Gln	Val	Thr	Arg	Glu	Asp	Asp	Gly	Ala	Ser	Ile	Val
					195			200				205			
Cys	Ser	Val	Asn	His	Glu	Ser	Leu	Lys	Gly	Ala	Asp	Arg	Ser	Thr	Ser
					210		215				220				
Gln	Arg	Ile	Glu	Val	Leu	Tyr	Thr	Pro	Thr	Ala	Met	Ile	Arg	Pro	Asp
					225		230			235			240		
Pro	Pro	His	Pro	Arg	Glu	Gly	Gln	Lys	Leu	Leu	Leu	His	Cys	Glu	Gly
					245				250				255		
Arg	Gly	Asn	Pro	Val	Pro	Gln	Gln	Tyr	Leu	Trp	Glu	Lys	Glu	Gly	Ser
					260			265				270			
Val	Pro	Pro	Leu	Lys	Met	Thr	Gln	Glu	Ser	Ala	Leu	Ile	Phe	Pro	Phe
					275				280			285			

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
 305 310 315 320

Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 85

gcttagaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 86

aacctggaaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 87		
cctagcacag tgacgaggga ctggc		26
<210> 88		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 88		
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc		50
<210> 89		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 89		
gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt		50
<210> 90		
<211> 2755		
<212> DNA		
<213> Homo sapiens		
<400> 90		
gggggttagg gaggaaggaa tccaccccca cccccccaaa cccttttttctt ctccctttcct 60		
ggcttcggac attggagcac taaatgaact tgaatttgtt ctgtggcgag caggatggtc 120		
gctgttactt tgtatgaga tcggggatga attgctcgct ttaaaaatgc tgctttggat 180		
tctgttgctg gagacgtctc tttgtttgc cgctggaaac gttacagggg acgtttgca 240		
agagaagatc tggccctgca atgagataga aggggaccta cacgtagact gtaaaaaaaaa 300		
gggcttcaca agtctgcagc gtttactgc cccgacttcc cagttttacc atttatttct 360		
gcatggcaat tccctcactc gactttccc taatgagttc gctaactttt ataatgcgg 420		
tagttgcac atggaaaaca atggcttgca taaaatcggtt ccgggggctt ttctgggct 480		
gcagctggtg aaaaggctgc acatcaacaa caacaagatc aagtctttc gaaagcagac 540		
ttttctgggg ctggacgatc tggaatatct ccaggctgtat ttaatttat tacgagatat 600		
agaccgggg gccttccagg acttgaacaa gctggagggtg ctcattttaa atgacaatct 660		
catcagcacc ctacctgcca acgtttcca gtatgtgccc atcacccacc tcgaccccg 720		
gggttaacagg ctgaaaacgc tgccttatga ggaggtcttg gagaaaaatcc ctggtatgtc 780		
ggagatcctg ctagaggata acccttggga ctgcacctgt gatctgtct ccctgaaaga 840		
atggctggaa aacattccca agaatgcct gatcggccga gtggctgcg aagccccac 900		
cagactgcag gttaaagacc tcaatgaaac caccgaacag gacttgtgtc ctttggaaaa 960		
ccgagtggat tctagtctcc cggcgcccc tggccaaagaa gagaccccttg ctccctggacc 1020		
cctgcacact ctttcaaga caaatggca agaggatcat gccacaccag ggtctgtcc 1080		

aaacggaggt acaaagatcc caggcaactg gcagatcaa atcagaccca cagcagcgat 1140
 agcgacgggt agctccagga acaaaccctt agctaacaat ttacccgtcc ctgggggttg 1200
 cagctgcac cacatcccag ggtcggttt aaagatgaac tgcaacaaca ggaacgtgag 1260
 cagctggct gatttgaagc ccaagctctc taacgtgcag gagctttcc tacgagataa 1320
 caagatccac agcatccgaa aatcgactt tgtggattac aagaacctca ttctgttgg 1380
 tctggcaac aataacatcg ctactgtaga gaacaacact ttcaagaacc ttttggacct 1440
 cagggtggcta tacatggata gcaattaccc ggacacgctg tccccggaga aattcgccgg 1500
 gctgcaaaac ctagagtacc tgaacgtgga gtacaacgct atccagctca tcctccggg 1560
 cacttcaat gccatgccca aactgaggat cctcattctc aacaacaacc tgctgagtc 1620
 cctgctgtg gacgtgttcg ctgggtctc gctctctaaa ctcagcctgc acaacaatta 1680
 cttcatgtac ctcccggtgg cagggtgtct ggaccaggta acctccatca tccagataga 1740
 cctccacgga aaccctggg agtgcctcg cacaattgtg ccttcaagc agtggggcaga 1800
 acgctgggt tccgaagtgc tgatgagcga cctcaagtgt gagacgcccgg tgaacttct 1860
 tagaaaggat ttcatgtcc ttcataatga cgagatctgc ctcagctgt acgcttagat 1920
 ctcgcccacg ttaacttcgc acagaaaaa cagcactggg ttggcggaga ccgggacgca 1980
 ctccaactcc tacctagaca ccagcagggt gtccatctcg gtgttgtcc cgggactgt 2040
 gctgggttt gtcacctccg cttcaccgt ggtgggcatg ctcgtgtta tcctgagaa 2100
 ccgaaagcgg tccaagagac gagatccaa ctcctcccg tccgagatta attccctaca 2160
 gacagtctgt gactcttcct actggcacaa tggccttac aacgcagatg gggcccacag 2220
 agtgtatgac tgtggctctc actcgctctc agactaagac cccaaacccca ataggggagg 2280
 gcagagggaa ggcgatacat cttcccccac cgcaggcacc ccggggcgtg gagggggcgtg 2340
 tacccaaatac cccgcgcct catcggat gggcataagt agataaataa ctgtgagctc 2400
 gcacaaccga aagggcctga ccccttactt agtccctcc ttgaaacaaa gagcagactg 2460
 tggagagctg ggagagcga gccagctcg tctttgctga gagcccctt tgacagaaag 2520
 cccagcacga ccctgctgaa agaactgaca gtgcctcg cctcggcccc ggggcctgtg 2580
 gggttggatg ccgcgggttc atacatatat acatatatcc acatctatat agagagatag 2640
 atatctattt ttccccgtg gattagcccc gtgtggctc cctgttgtt acgcaggat 2700
 gggcagttgc acgaaggcat gaatgtattt taaaataagta actttgactt ctgac 2755

<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

Met	Leu	Leu	Trp	Ile	Leu	Leu	Glu	Thr	Ser	Leu	Cys	Phe	Ala	Ala
1														15

Gly	Asn	Val	Thr	Gly	Asp	Val	Cys	Lys	Glu	Lys	Ile	Cys	Ser	Cys	Asn
20															30

Glu	Ile	Glu	Gly	Asp	Leu	His	Val	Asp	Cys	Glu	Lys	Lys	Gly	Phe	Thr
35															45

Ser	Leu	Gln	Arg	Phe	Thr	Ala	Pro	Thr	Ser	Gln	Phe	Tyr	His	Leu	Phe
50															60

Leu	His	Gly	Asn	Ser	Leu	Thr	Arg	Leu	Phe	Pro	Asn	Glu	Phe	Ala	Asn
65															80

Phe	Tyr	Asn	Ala	Val	Ser	Leu	His	Met	Glu	Asn	Asn	Gly	Leu	His	Glu
85															95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
 100 105 110

Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
 115 120 125

Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp
 130 135 140

Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile
 145 150 155 160

Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
 165 170 175

Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu
 180 185 190

Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu
 195 200 205

Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys
 210 215 220

Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val
 225 230 235 240

Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr
 245 250 255

Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
 260 265 270

Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr
 275 280 285

Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala
 290 295 300

Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg
 305 310 315 320

Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala
 325 330 335

Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly
 340 345 350

Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala
 355 360 365

Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp
 370 375 380

Asn	Lys	Ile	His	Ser	Ile	Arg	Lys	Ser	His	Phe	Val	Asp	Tyr	Lys	Asn
385					390					395					400
Leu	Ile	Leu	Leu	Asp	Leu	Gly	Asn	Asn	Ile	Ala	Thr	Val	Glu	Asn	
				405					410				415		
Asn	Thr	Phe	Lys	Asn	Leu	Leu	Asp	Leu	Arg	Trp	Leu	Tyr	Met	Asp	Ser
		420						425					430		
Asn	Tyr	Leu	Asp	Thr	Leu	Ser	Arg	Glu	Lys	Phe	Ala	Gly	Leu	Gln	Asn
		435				440						445			
Leu	Glu	Tyr	Leu	Asn	Val	Glu	Tyr	Asn	Ala	Ile	Gln	Leu	Ile	Leu	Pro
		450			455					460					
Gly	Thr	Phe	Asn	Ala	Met	Pro	Lys	Leu	Arg	Ile	Leu	Ile	Leu	Asn	Asn
		465			470				475					480	
Asn	Leu	Leu	Arg	Ser	Leu	Pro	Val	Asp	Val	Phe	Ala	Gly	Val	Ser	Leu
		485					490						495		
Ser	Lys	Leu	Ser	Leu	His	Asn	Asn	Tyr	Phe	Met	Tyr	Leu	Pro	Val	Ala
		500					505						510		
Gly	Val	Leu	Asp	Gln	Leu	Thr	Ser	Ile	Ile	Gln	Ile	Asp	Leu	His	Gly
		515				520						525			
Asn	Pro	Trp	Glu	Cys	Ser	Cys	Thr	Ile	Val	Pro	Phe	Lys	Gln	Trp	Ala
		530				535						540			
Glu	Arg	Leu	Gly	Ser	Glu	Val	Leu	Met	Ser	Asp	Leu	Lys	Cys	Glu	Thr
		545			550				555					560	
Pro	Val	Asn	Phe	Phe	Arg	Lys	Asp	Phe	Met	Leu	Leu	Ser	Asn	Asp	Glu
			565					570					575		
Ile	Cys	Pro	Gln	Leu	Tyr	Ala	Arg	Ile	Ser	Pro	Thr	Leu	Thr	Ser	His
			580				585						590		
Ser	Lys	Asn	Ser	Thr	Gly	Leu	Ala	Glu	Thr	Gly	Thr	His	Ser	Asn	Ser
			595			600						605			
Tyr	Leu	Asp	Thr	Ser	Arg	Val	Ser	Ile	Ser	Val	Leu	Val	Pro	Gly	Leu
		610				615					620				
Leu	Leu	Val	Phe	Val	Thr	Ser	Ala	Phe	Thr	Val	Val	Gly	Met	Leu	Val
		625			630				635					640	
Phe	Ile	Leu	Arg	Asn	Arg	Lys	Arg	Ser	Lys	Arg	Arg	Asp	Ala	Asn	Ser
			645					650					655		
Ser	Ala	Ser	Glu	Ile	Asn	Ser	Leu	Gln	Thr	Val	Cys	Asp	Ser	Ser	Tyr

660	665	670
Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp		
675	680	685
Cys Gly Ser His Ser Leu Ser Asp		
690	695	
<210> 92		
<211> 22		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 92		
gttggatctg ggcaacaata ac		22
<210> 93		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 93		
attgttgtgc aggctgagtt taag		24
<210> 94		
<211> 45		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 94		
ggtggtata catggatagc aattacctgg acacgctgtc ccgggg		45
<210> 95		
<211> 2226		
<212> DNA		
<213> Homo sapiens		
<400> 95		
agtgcactgc gtcccctgta cccggcgcca gctgtgttcc tgaccccaga ataactcagg 60		
gctgcaccgg gcctggcagc gctccgcaca catttcctgt cgccgcctaa gggaaactgt 120		
tggccgctgg gccccgggg ggattcttgg cagttggggg gtccgtcggg agcgaggcg 180		

ggggggaaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgt 240
ccagacacag ctctgcgtcc tcgagcgaaa cagatccaag ttgggagcag ctctgcgtgc 300
ggggcctcag agaatgaggg cggcgttcgc cctgtgcctc ctctggcagg cgctctggcc 360
ccccccgggc ggcggcgaac accccactgc cgaccgtgtc ggctgctgg cctcgaaaa 420
ctgctacagc ctgcaccacg ctaccatgaa gcggcaggcg gcccaggagg cctgcattcct 480
gcgagggtggg gcgctcagca ccgtgcgtgc gggcgccgag ctgcgcgtg tgctcgcgt 540
cctgcgggca ggcggcgggc cggaggggg ctccaaagac ctgtgtttt gggcgcact 600
ggagcgcagg cgttccact gcaccctgga gaacgagcc ttgcggggt ttcctggct 660
gtcctccgac cccggcggtc tcgaaagcga cacgctgcag tgggtggagg agccccaaacg 720
ctcctgcacc gcgcggagat gcgcgtact ccaggccacc ggtgggtcg agccgcagg 780
ctggaaggag atgcgatgcc acctgcgcgc caacggctac ctgtgcaagt accagttga 840
ggtcttgtt cctgcgcccgc gccccggggc cgccctctaacc ttgagctatc gcgcgcctt 900
ccagctgcac agcgcgcgtc tggacttcag tcacacctggg accgaggtga gtgcgcctcg 960
ccggggacag ctccccatct cagttacttg catcgccgac gaaatcgcc ctcgcgtgg 1020
caaactctcg ggcgatgtgt tgtgtccctg ccccgggagg tacccctgt ctggcaaatg 1080
cgcagagctc cctaactgcc tagacgactt gggaggctt gcctgcgaat gtgcgtacggg 1140
cttcgagctg gggaggacgc gccgcttgc tggaccatg ggggaaggac agccgaccct 1200
tggggggacc ggggtgccc ccaggccccc gccggccact gcaaccagcc cctgcgcgc 1260
gagaacatgg ccaatcaggg tcgacgagaa gotgggagag acaccacttgc tccctgaaca 1320
agacaattca gtaacatcta ttccctgagat tcctcgatgg ggatcacaga gcacgatgtc 1380
tacccttcaa atgtcccttc aagccgagtc aaaggccact atcacccat cagggagcgt 1440
gatttccaag tttatttcta cgacttcctc tgccactcct caggcttcg actcctccctc 1500
tgccgtggtc ttcatatatttgc tgagcacagc agtagtagtg ttggtagatc tgaccatgac 1560
agacttgggg ctgtcaagc tctgcattca cggaaagcccc tttcccaagc caaggaagga 1620
gtctatgggc cccggggcc tggagagtga tcctgagcc gctgcattgg gctccagtc 1680
tgcacattgc acaaacaatg gggtaaaatg cggggactgt gatctgcggg acagagcaga 1740
gggtgccttgc ctggcgagg cccctttgg ctcttagtgat gcatagggaa acaggggaca 1800
tgggcactcc tggtaacatgt ttctactt tgatgaaaacg gggaaaccaag aggaacttac 1860
ttgtgttaact gacaatttct gcagaaatcc cccttcctt aaattccct tactccactg 1920
aggagctaaa tcagaactgc acactccctc cctgtatgata gaggaagtgg aagtgcctt 1980
aggatggta tactggggc cgggttagtg ctggggagag atatttctt atgtttattc 2040
ggagaatttg gagaagtgtat tgaactttc aagacattgg aaacaaatag aacacaat 2100
aatttacatt aaaaaataat ttctacccaa atggaaagga aatgttctat gttgttcagg 2160
ctaggagtat attggttcga aatccccaggg aaaaaaaaataa aaataaaaaaaa ttaaaggatt 2220
gttgat 2226

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
1 5 10 15

Gly Pro Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly
 65 70 75 80
 Pro Gly Pro Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu
 85 90 95
 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly
 100 105 110
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu
 115 120 125
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala
 130 135 140
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met
 145 150 155 160
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu
 165 170 175
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr
 180 185 190
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro
 195 200 205
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val
 210 215 220
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly
 225 230 235 240
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys
 245 250 255
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu
 260 265 270
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr
 275 280 285
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg
 290 295 300
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro
 305 310 315 320
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln
 325 330 335
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

340	345	350
Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala		
355	360	365
Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr		
370	375	380
Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe		
385	390	395
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr		
405	410	415
Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln		
420	425	430
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu		
435	440	445
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val		
450	455	460
Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu		
465	470	475
Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala		
485	490	

<210> 97

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 97

tggaaggaga tgcgatgccca cctg

24

<210> 98

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 98

tgaccagtgg ggaaggacag

20

<210> 99		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 99		
acagagcaga gggtgccattg		20
<210> 100		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 100		
tcaggcacaa gtgggtctc tccc		24
<210> 101		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 101		
tcagggaagg agtgtgcagt tctg		24
<210> 102		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 102		
acagctcccc atctcagtta cttgcattgc ggacgaaatc ggcgctcgct		50
<210> 103		
<211> 2026		
<212> DNA		
<213> Homo sapiens		

<400> 103

cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagccctca gggaaacta 60
 agcgtcgagt cagacggcac cataatcgcc tttaaaagtg cctccgcctt gccggcccg 120
 tatccccgg ctacctgggc cgccccggc cggtgtcgcc gtgagaggga gcgcgcggc 180
 agccgagcgc cggtgtgagc cagcgtgtc gccagtgtgta gcggcggtgt gagcgcggtg 240
 ggtgcggagg ggcgtgtgt ccggcgcgcg cgccgtgggg tgcaaaccac 300
 gctgccatga ggggcgcgaa cgcctggcg ccactctgcc tgctgtggc tgccgcacc 360
 cagctctcgcc ggcagcgtc cccagagaga cctgtttca catgtggtgg cattcttact 420
 ggagagtctg gatttattgg cagtgaaggt ttcctggag tgtaccctcc aaatagcaaa 480
 tgtacttggaa aatcacagt tcccgaagga aaagtagtgc ttctcaattt ccgattcata 540
 gacacgcgaga gtgacaacct gtgccgtat gactttgtgg atgtgtacaa tggccatgcc 600
 aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgggtccagt 660
 ggcaacaaga tggatgtgca gatgatttct gatgccaaca cagctggcaa tggcttcatg 720
 gccatgttct cgcgtgtga accaaacgaa agaggggatc agtattgtgg aggactcctt 780
 gacagacatt cccgctctt taaaaccccc aactggccag accgggatta ccctgcagga 840
 gtcacttgc tgggtcacat tggatgttca aagaatcgc ttatagaatt aaagtttgag 900
 aagtttgcatttgc tggagcgaga taactactgc cgatatgatt atgtggctgt gtttatggc 960
 ggggaagtca acgatgttag aagaatttggaa aagtattgtg gtgatagtc acctgcgc 1020
 atttgtctg agagaaatgaa acttcttatt cagttttat cagacttaag tttaactgca 1080
 gatgggttta ttggactca catattcagg ccaaaaaaac tgcctacaac tacagaacag 1140
 cctgtcacca ccacattccc tggatgttca accaaacgaa agggggatc agtattgtgg 1200
 caaaaatgttca gacggacggg gactctggag ggcaattatt gttcaagtga ctttgttata 1260
 gcccgcactg ttatcacaac catcaactgc gatgggagtt tgcacgccc acgtctcgatc 1320
 atcaacatct acaaagaggg aaatttggcg attcagcagg cgggcaagaa catgagtgcc 1380
 aggctgactg tcgtctgc gcaatgttca accaaacgaa aggggttcaaa ttacatttatt 1440
 atgggcaag taggtgaaga tggcgaggc aaaatcatgc caaacagctt tatcatgtatg 1500
 ttcaagacca agaatttggcg gtccttggat gcctaaaaaa ataagcaatg ttaacagtga 1560
 actgtgtcca tttaagctgt attctgcatt tgccttggat agatctatgt tctctcgtt 1620
 gaaaaaaaaa tacttataaa attacatatt tggatgttca accaaacgaa agggggactgg 1680
 ttgactcttcc acatgtatggaa ggtatgtggc ctccgagata gctggggaa gttcttgc 1740
 tgctgtcaga ggagcagcta tctgatttgc aacctgcgca ctttgtggc tgataggaag 1800
 ctaaaatgttca gacggacggg gactctggag ggcaattatt atacatctt gtaaaaggat 1860
 attttagaat tgagttgtgt gaagatgtca aaaaaagatt tttagtgc aatatttata 1920
 gtgttatttgc ttgcacccgc aaccttgc ctttgtggc tgataggaag 1980
 tctaaatcaa tgcttataaa aatatttttgc aaggaaaaaaa aaaaaaa 2026

<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

Met	Arg	Gly	Ala	Asn	Ala	Trp	Ala	Pro	Leu	Cys	Leu	Leu	Leu	Ala	Ala
1								10						15	

Ala	Thr	Gln	Leu	Ser	Arg	Gln	Gln	Ser	Pro	Glu	Arg	Pro	Val	Phe	Thr
								20		25			30		

Cys	Gly	Gly	Ile	Leu	Thr	Gly	Glu	Ser	Gly	Phe	Ile	Gly	Ser	Glu	Gly
								35		40			45		

Phe	Pro	Gly	Val	Tyr	Pro	Pro	Asn	Ser	Lys	Cys	Thr	Trp	Lys	Ile	Thr
								50		55			60		

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
 65 70 75 80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
 85 90 95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
 100 105 110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
 115 120 125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
 130 135 140

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg
 145 150 155 160

Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
 165 170 175

Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
 180 185 190

Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
 195 200 205

Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
 210 215 220

Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
 225 230 235 240

Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
 245 250 255

Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
 260 265 270

Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Phe Pro Val Thr Thr
 275 280 285

Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
 290 295 300

Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly
 305 310 315 320

Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
 325 330 335

Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

340

345

350

Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro
 355 360 365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu
 370 375 380

Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys
 385 390 395 400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys
 405 410 415

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 105

ccgatttcata gacctcgaga gt

22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac

22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108

<211> 1838

<212> DNA

<213> Homo sapiens

<400> 108

cgacgcgtg ggccggacgcg tggcgggccc acggcgcccg cggctgggg cggtcgcttc 60
 ttccttctcc gtggcctacg agggtccccca gcctggtaa agatggccccc atggccccc 120
 aaggccttag tcccagctgt gctctgggc ctcagcctct tcctcaacct cccaggac 180
 atctggctcc agccctctcc acctcccccag tcttctccccc cgcctcagcc ccatccgtgt 240
 cataacctgcc ggggactggt tgacagctt aacaaggccc tggagagaac catccggac 300
 aactttggag gtggaaacac tgcctggag gaagagaatt tgtccaaata caaagacagt 360
 gagacccgccc tggtagaggt gctggagggt gtgtcagca agtcaagactt cgagtgcac 420
 cgcctgctgg agctgagtga ggagctgggag gagagctgggat gtttcacaa gcagcaggag 480
 gccccggacc tcttcagtg gctgtgctca gattccctga agctctgctg ccccgccaggc 540
 accttcgggc ctcctgcct tccctgtcct gggggAACAG agagccctg cggtggctac 600
 gggcagtgtg aaggagaagg gacacgagggg ggcagcgggc actgtgactg ccaagccggc 660
 tacgggggtg aggccctgtgg ccagtggtgc ctggctact ttgaggcaga acgcaacgcc 720
 agccatctgg tatgttcggc ttgtttggc ccctgtgccc gatgctcagg acctgagaa 780
 tcaaactgtt tgcaatgc当地 gaaggcgtgg gccctgcatac acctaactgt tgtagacatt 840
 gatgagtgtg gcacagagggg agccaactgt ggagctgacc aattctgcgt gaacactgag 900
 ggctcctatg agtgcgaga ctgtgccaag gcctgcctag gctgcataggg ggcaggccca 960
 ggtcgctgta agaagtgttag ccctggctat cagcagggtgg gctccaagtg tctcgatgtg 1020
 gatgagtgtg agacagaggt gtgtccgggaa gagaacaagc agtgtgaaaa caccgaggc 1080
 ggttatcgct gcatctgtgc cgagggtctac aagcagatgg aaggcatctg tgtgaaggag 1140
 cagatcccag agtcagcagg cttcttctca gagatgacag aagacgagtt ggtggctgtg 1200
 cagcagatgt tctttggcat catcatctgt gcactggcca cgctggctgc taagggcgc 1260
 ttgggttca cgcgcattt cattgggct gtggcggcca tgactggcta ctgggttca 1320
 gagcgcagtg accgtgtgct ggagggtctc atcaaggcataa gataatcgcg gccaccac 1380
 gtaggacctc ctccccacca cgctgcccccc agagctggg ctggccctct gctggacact 1440
 caggacagct tggtttattt ttgagagtgg ggtaaaggcacc cctacctgccc ttacagagca 1500
 gcccaggtaa ccaggccccgg gcagacaagg cccctggggaaa aaaaagtagc cctgaagggt 1560
 gataccatga gctttcacc tggcggggac tggcagggtt cacaatgtgt gaatttcaaa 1620
 agttttcct taatggtggc tgctagagct ttggccctgt ctttaggatta ggtggtcctc 1680
 acaggggtgg ggccatcaca gtccttcctt gccagctgca tgctgcccagt tcctgttctg 1740
 tgttcaccac atccccacac cccattgcca cttatttattt catctcagga aataaagaaa 1800
 ggtcttgaa agttaaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

Met	Ala	Pro	Trp	Pro	Pro	Lys	Gly	Leu	Val	Pro	Ala	Val	Leu	Trp	Gly
1															

5

10

15

Leu	Ser	Leu	Phe	Leu	Asn	Leu	Pro	Gly	Pro	Ile	Trp	Leu	Gln	Pro	Ser
20															

25

30

Pro	Pro	Pro	Gln	Ser	Ser	Pro	Pro	Pro	Gln	Pro	His	Pro	Cys	His	Thr
35															

40

45

Cys	Arg	Gly	Leu	Val	Asp	Ser	Phe	Asn	Lys	Gly	Leu	Glu	Arg	Thr	Ile
50															

55

60

Arg Asp Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu
 65 70 75 80

Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
 85 90 95

Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
 100 105 110

Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
 115 120 125

Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
 130 135 140

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu
 145 150 155 160

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly
 165 170 175

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Glu Ala Cys
 180 185 190

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His
 195 200 205

Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro
 210 215 220

Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His
 225 230 235 240

Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys
 245 250 255

Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg
 260 265 270

Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg
 275 280 285

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu
 290 295 300

Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln
 305 310 315 320

Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr
 325 330 335

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala
 340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
 405 410 415

Ile Lys Gly Arg
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaaagtgt ctcgatgtgg atgagtgtga

50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 112

atctgcttgt agccctcgcc ac

22

<210> 113

<211> 1616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1461)
 <223> a, t, c or g

<400> 113
 tgagaccctc ctgcagccctt ctcaaggac agccccactc tgcctttgc tcctccaggg 60
 cagcaccatg cagccccgt ggcctctgt ggcaactctgg gtgttgcggg tggccagccc 120
 cggggccgccc ctgaccgggg agcagctcct gggcagccctg ctgcggcagc tgcagctcaa 180
 agaggtgtccc accctggaca gggccgacat ggaggagctg gtcattccca cccacgttag 240
 ggcccagtac gtggccctgc tgcagcgcac ccacggggac cgctcccgcg gaaagaggtt 300
 cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360
 gctgggtttc ggcattggac agcggctgcc gcccaacagc gagctggtgc aggccgtgt 420
 gcggtcttc caggagccgg tccccaaaggc cgccgtgcac aggcaacggc ggctgtcccc 480
 gcgccagccccc cggggccccc tgaccgtcga tgccgtgcgc gtccggcagc acggctccaa 540
 cccgacccctcc ctcatcgact ccaggctggt gtccgtccac gagagcggct ggaaggccctt 600
 cgacgtgacc gaggccgtga acttctggca gcaagctgagc cggcccccggc agccgctgt 660
 gctacaggtg tcgggtcaga gggagcatct gggcccgctg gcgtccggcg cccacaagct 720
 ggtccgtttt gctcgcagg gggccggcagc cgggcttggtt gagcccccagc tggagctgca 780
 caccctggac ctggggact atggagctca gggcgactgt gaccctgaag caccaatgac 840
 cgagggcacc cgctgtgcc gccaggagat gtacattgac ctgcagggga tgaagtgggc 900
 cgagaactgg gtgctggagc ccccgccctt cctggcttat gagtgtgtgg gcacctgccc 960
 gcagccccccg gaggccctgg ccttcaagtg gccgtttctg gggccctcgac agtgcac 1020
 ctggagact gactcgctgc ccatgatcgat cagcatcaag gagggaggca gaccaggccc 1080
 ccaggtggtc agcctgccc acatgagggt gcagaagtgc agctgtgcct cggatggtgc 1140
 gctcgccca aggaggctcc agccataggc gcctagtgta gccatcgagg gacttgactt 1200
 gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gcatgactg aactgctgat 1260
 ggacaaatgc tctgtgtct ctatgtgac ccgtatgttgc ttccctgtac aagttacctc 1320
 acctaatttt tgcttctcag gaatgagaat ctttggccac tggagagccc ttgctcagg 1380
 ttctcttattc ttattattca ctgcactata ttcttaagcac ttacatgtgg agatactgta 1440
 acctgagggc agaaaagccc ntgtgtcatt gtttacttgt cctgtcaactg gatctgggt 1500
 aaagtctcc accaccactc tggaccctaa acctgggggtt aagtgtgggt tgcgtcatccc 1560
 caatccagat aataaaagact ttgtaaaaaca tgaataaaac acattttattt ctaaaa 1616

<210> 114
 <211> 366
 <212> PRT
 <213> Homo sapiens

<400> 114
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala
 1 5 10 15

Ser	Pro	Gly	Ala	Ala	Leu	Thr	Gly	Gln	Leu	Leu	Gly	Ser	Leu	Leu
20								25					30	

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
 35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
 50 55 60

Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
 65 70 75 80

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
 85 90 95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
 100 105 110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
 115 120 125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
 130 135 140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
 145 150 155 160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
 165 170 175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
 180 185 190

Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
 195 200 205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
 210 215 220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
 225 230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
 245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
 260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
 275 280 285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
 290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
 305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
 355 360 365

<210> 115
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 115
 aggactgccca taacttgcct g 21

<210> 116
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 116
 ataggagttg aaggcagcgct gc 22

<210> 117
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 117
 tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118
<211> 1857
<212> DNA
<213> Homo sapiens

<400> 118
 gtctgttccc aggagtcctt cggccgctgt tgtgtcagtgc ctcttcatat tggcgatcct gttgtgtcc 60
 aaggcgcaag tcgagaggaa actgttgtgc 120
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcaaat tcctgagaat 180

aatcctgtga agttgcctcg tgccactactcg ggctttctt ctcgggtgt ggagtgaaag 240
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300
gaggaccggg tgacccctt gccaactggg atcacctca agtccgtgac acggaaagac 360
actgggacat acaattgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctccctgtcc 480
accattgggaa accgggcagt gctgacatgc tcagaacaag atggttcccc accttctgaa 540
tacacctggg tcaaagatgg gatagtgtat cctacgaatc ccaaagcac ccgtgccttc 600
agcaactctt cctatgtctt gaatccocaca acaggagagc tggtcttga tccctgtca 660
gcctctgata ctggagaata cagctgtgag gcacggaaatg ggtatggac acccatgact 720
tcaaatgctg tgcgcattggg agctgtggg cgaatgtgg gggcatogt ggcagccgtc 780
cttgcataacc tgattctcctt gggaaatctt gtttttggca tctgggttgc ctatagccga 840
ggccactttg acagaacaaa gaaaggact tcgagtaaga aggtgattt cagccagcct 900
agtgcggaa gtgaaggaga attcaaacag acctcgcat tcctgggtg agcctggtcg 960
gctcaccggcc tatcatctgc attgcctt ctcagggtgc accggactct gcccctgtat 1020
gtctgttagtt tcacaggatg ctttatttgc ttctcacacc ccacagggcc ccctactt 1080
tcggatgtgt ttttataat gtcagctatg tgccccatcc tccttcatgc ctcctctccc 1140
tttccttacca ctgctgagtg gcctggaaact tggtaaaatg gtttattccc catttcttt 1200
aggatcagg aaggaatcct gggatgcca ttgacttccc ttctaagtag acagaaaaaa 1260
tggcgggggt cgaggaaatc tgcaactcaac tgccccacctg gctggcaggg atctttgaat 1320
aggtatctt agttggttc tgggctttt ctttgttac tgacgaccag gccagctgt 1380
tctagagcgg gaatttagagg ctagagcggc tggaaatgggt gtttgggtat gacactgggg 1440
tccttcacat tctggggccc actctttct gtcttccat gggaaatgcc actgggatcc 1500
ctctgccttgc tcctcctgaa tacaagctga ctgacattga ctgtgttgt gaaaaatggg 1560
agctctgtt gtggagagca tagtaaaat tcaagagaact tgaagccaaa aggatttaaa 1620
accgctgctc taaagaaaaag aaaactggag gctgggcgcga gtggctcacg cctgtatcc 1680
cagaggctga ggcaggcggc tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
ggagaaaaccc tactggaaat acaaagtttgc ccaggcatgg tggtgcatgc ctgttagtccc 1800
agctgctcag ggcctggca acaagagcaa aactccagct caaaaaaaaaaaaaaaa 1857

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
 165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
 180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
 195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
 210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Gly Ile Leu Val Phe Gly
 245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
 260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
 275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 120

tgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 121
tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50

<210> 122
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 122
acacacctggtt caaagatggg 20

<210> 123
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 123
taggaagagt tgctgaaggc acgg 24

<210> 124
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 124
ttgccttact caggtgctac 20

<210> 125
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 125
 actcagcagt ggttagaaag 20

 <210> 126
 <211> 1210
 <212> DNA
 <213> Homo sapiens

 <400> 126
 cagcgcgtgg ccggcgccgc tgtgggaca gcatgagcgg cggttggatg ggcagggttg 60
 gagcgtggcg aacaggggct ctgggcctgg cgctgctgt gctgctcggc ctcggactag 120
 gcctggagggc cggccgcgagc cccgcaccc tggccaggcc gcaggcccc 180
 gctcaggctc gtgcccaccc accaagtcc agtgcgcac cagtggcta tgcgtgcccc 240
 tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgca 300
 ggattgagcc atgtacccag aaaggcaat gcccaccgccc ccctggcctc ccctgccc 360
 gcaccggcgt cagtgaactgc tctggggaa ctgacaagaaa actgcgcac acgcggcc 420
 tggcctgcct agcaggcgag ctccggtgca cgctgagcga tgactgcatt ccactcacgt 480
 ggcgtgcga cggccaccca gactgtccc actccagcga cgagctggc tggaaacca 540
 atgagatcct cccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagatg 600
 tcacctctc caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgcctcc 660
 ctgtcggaa tgccacatcc tcctctgccc gagaccagtc tggaagccca actgcctatg 720
 gggttattgc agtgcgtgcg gtgcctagtg caagcctggt caccgcacc ctcctcctt 780
 tgtcctggct cggagccca gagegcctcc gcccactggg gttactggg gccatgaagg 840
 agtccctgct gtcgtcagaa cagaagaccc cgctgcctg aggacaagca cttgcccacca 900
 ccgtcactca gcccctggcg tagccggaca ggaggagagc agtgcgtgcg atgggtaccc 960
 gggcacacca gcccctcagag acctgagttc ttctggccac gtggAACCTC gaaccggagc 1020
 tcctgcagaa gtggccctgg agattggggg tccctggaca ctccctatgg agatccgggg 1080
 agcttaggatg gggAACCTGC cacagccaga actgaggggc tggcccccagg cagctccca 1140
 ggggtagaac gcccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgattt 1200
 aagttgcttc 1210

 <210> 127
 <211> 282
 <212> PRT
 <213> Homo sapiens

 <400> 127
 Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
 1 5 10 15

 Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
 20 25 30

 Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
 35 40 45

 Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
 50 55 60

 Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
 65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
 85 90 95

Lys Gly Gln Cys Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
 100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
 115 120 125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
 130 135 140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
 145 150 155 160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
 165 170 175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
 180 185 190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
 195 200 205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
 210 215 220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala
 225 230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln
 245 250 255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
 260 265 270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
 275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

24

<210> 129

cggcaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200
 agttcaaggc ccactttccc cccagggggc ctcggcggag ttccagcagt gaccctgact 1260
 ttgtgggtt agacggcggtg cccgtcatgc tccccgtccta tgacgaagct gtgagtgccg 1320
 gctttagtgc cttagggccc gggtacatgg cctctgtggg ccagggtgc cccttacccg 1380
 tggacacca gagcccccca gcataccccc gtcaggggc cacggacaca ggcccagggg 1440
 agtcagaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500
 ctcccagggtg ccaagagagc acccaccctg cttcggacaa ccctgacata attgccagca 1560
 cggcagagga ggtggcatcc accagcccag gcatccatca tgcccaactgg gtgttgtcc 1620
 taagaaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680
 gttgatctgt ggagttgatt ctttccttc tcttggttt agacaaatgt aaacaaagct 1740
 ctgatccta aaattgctat gctgatagag tggtagggc tggaagctg atcaagtct 1800
 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met	Tyr	His	Gly	Met	Asn	Pro	Ser	Asn	Gly	Asp	Gly	Phe	Leu	Glu	Gln
1														15	

Gln	Gln	Gln	Gln	Gln	Pro	Gln	Ser	Pro	Gln	Arg	Leu	Leu	Ala	Val
													30	
20					25									

Ile	Leu	Trp	Phe	Gln	Leu	Ala	Leu	Cys	Phe	Gly	Pro	Ala	Gln	Leu	Thr
															45
35					40										

Gly	Gly	Phe	Asp	Asp	Leu	Gln	Val	Cys	Ala	Asp	Pro	Gly	Ile	Pro	Glu
															60
50					55										

Asn	Gly	Phe	Arg	Thr	Pro	Ser	Gly	Gly	Val	Phe	Phe	Glu	Gly	Ser	Val
															80
65					70					75					

Ala	Arg	Phe	His	Cys	Gln	Asp	Gly	Phe	Lys	Leu	Lys	Gly	Ala	Thr	Lys
															95
85					90										

Arg	Leu	Cys	Leu	Lys	His	Phe	Asn	Gly	Thr	Leu	Gly	Trp	Ile	Pro	Ser
															110
100					105										

Asp	Asn	Ser	Ile	Cys	Val	Gln	Glu	Asp	Cys	Arg	Ile	Pro	Gln	Ile	Glu
															125
115					120										

Asp	Ala	Glu	Ile	His	Asn	Lys	Thr	Tyr	Arg	His	Gly	Glu	Lys	Leu	Ile
															140
130					135										

Ile	Thr	Cys	His	Glu	Gly	Phe	Lys	Ile	Arg	Tyr	Pro	Asp	Leu	His	Asn
															160
145					150				155						

Met	Val	Ser	Leu	Cys	Arg	Asp	Asp	Gly	Thr	Trp	Asn	Asn	Leu	Pro	Ile
															175
165					170										

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

180	185	190
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr		
195	200	205
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys		
210	215	220
Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu		
225	230	235
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe		
245	250	255
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val		
260	265	270
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr		
275	280	285
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys		
290	295	300
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr		
305	310	315
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu		
325	330	335
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His		
340	345	350
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Asp Pro Asp Phe		
355	360	365
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala		
370	375	380
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val		
385	390	395
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr		
405	410	415
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys		
420	425	430
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro		
435	440	445
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile		
450	455	460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn
 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 133

atctccatac gctgcttcc cggt

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttacaa aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

ccccacgcgtc cgctccgcgc cctccccccc gcctcccggtg cggccgcgtcg gtggccctaga 60

gatgctgctg ccgcgggttgc agttgtcgcg cacgcctctg cccggccagcc cgctccacccg 120

ccgttagcgcgc cgagtgtcggt gggggcgcacc cgagtccggc catgaggccg ggaaccgcgc 180

tacagggccgt gctgctggcc gtgctgctgg tggggctgctg ggccgcgcacg ggtcgcctgc 240

tgagtgcctc ggatttggac ctcagaggag ggcagccagt ctgccgggga gggacacacaga 300

ggccttgtta taaaagtatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
 ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
 agaaaactgat agaaaagtcc attgaaaacc tcttgccatc tgatgggtac ttctggattg 480
 ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgcaggac ctttatgctt 540
 ggactgtatgg cagcatatca caatttagga actgttatgt ggatgagccg tcctgcggca 600
 gcgaggctcg cgtggtcatg taccatcagc catcgccacc cgctggcatc ggaggcccct 660
 acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaataatt 720
 ctgtatgagaa accagcagg tcttcagag aagctgaagg tgagaaaca gagctgacaa 780
 cacctgtact tccagaagaa acacaggaag aagatgcca aaaaacattt aaagaaagta 840
 gagaagctgc cttgaatctg gcctacatcc taatccccag cattccctt ctccctcc 900
 ttgtgtcac cacagttgtt tggtgggtt ggatctgtag aaaaagaaaa cgggagcagc 960
 cagaccttag cacaagaag caacacacca tctggccctc tcctcaccag gaaaacagcc 1020
 cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080
 gGCCAGACCT gaagaatatt tcattccgag tgggttgcgg agaagccact cccgatgaca 1140
 tgtctgtga ctatgacaac atggctgtga acccatcaga aagtgggtt gtgactctgg 1200
 tgagcgtgga gagtggatt gtgaccaatg acatttatga gttctccca gaccaaataatgg 1260
 ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaaa 1320
 aaactgaaac tgacaacaat gaaaaagaaaa tgataagoaa aatctctta ttttctataa 1380
 gaaaaataca cagaaggct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440
 tccccacgac ctctgttgg acccccacgt tttggctgta tccttctatcc cagccagtc 1500
 tccagctcg ccttatgaga aggtacctt cccaggtctg gcacatagta gagtctcaat 1560
 aaatgtcaact tggttggttg tatctaactt ttaagggaca gagcttacc tggcagtgtat 1620
 aaagatgggc tggagctt gaaaaaccac ctctgtttc ctgctctat acagcagcac 1680
 atattatcat acagacagaa aatccagaat ctttcaaag cccacatatg gtagcacagg 1740
 ttggctgtg catcgcaat tctcatatct gttttttca aagaataaaa tcaaataaaag 1800
 agcagaaaaa aaaaaa 1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met	Arg	Pro	Gly	Thr	Ala	Leu	Gln	Ala	Val	Leu	Leu	Ala	Val	Leu	Leu
1									10					15	

Val	Gly	Leu	Arg	Ala	Ala	Thr	Gly	Arg	Leu	Leu	Ser	Ala	Ser	Asp	Leu
									25					30	

Asp	Leu	Arg	Gly	Gly	Gln	Pro	Val	Cys	Arg	Gly	Gly	Thr	Gln	Arg	Pro
									40				45		

Cys	Tyr	Lys	Val	Ile	Tyr	Phe	His	Asp	Thr	Ser	Arg	Arg	Leu	Asn	Phe
													50		55

Glu	Glu	Ala	Lys	Glu	Ala	Cys	Arg	Arg	Asp	Gly	Gly	Gln	Leu	Val	Ser
													65		70

Ile	Glu	Ser	Glu	Asp	Glu	Gln	Lys	Leu	Ile	Glu	Lys	Phe	Ile	Glu	Asn
									85				90		95

Leu	Leu	Pro	Ser	Asp	Gly	Asp	Phe	Trp	Ile	Gly	Leu	Arg	Arg	Glu	
									100				105		110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
 115 120 125
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
 130 135 140
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
 145 150 155 160
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
 165 170 175
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
 180 185 190
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
 195 200 205
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
 210 215 220
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
 225 230 235 240
 Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
 245 250 255
 Trp Ile Cys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
 260 265 270
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
 275 280 285
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
 290 295 300
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly
 305 310 315 320
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
 325 330 335
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
 340 345 350
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
 355 360 365
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr
 370 375 380

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 138
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 139
 aagccaaaga agcctgcagg aggg 24

<210> 140
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 140
 cagtccaagc ataaagggtcc tggc 24

<210> 141
 <211> 1514
 <212> DNA
 <213> Homo sapiens

<400> 141
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60
 gcatccgcag gttcccgccg acttgggggc gcccgcgtgag ccccgccgcgccc cgcaaaagac 120
 ttgtgtttgc ctccctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180
 tggtgtgttc agcatgcgtct tgtggacccc agtgggcgtc ctgacccctgc tggcgtactg 240
 cctgcaccag cggcggtgg ccctggccga gctgcaggag gccgatggcc agtgtccgg 300
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggtcggt tttcgacacg gggctcgag 360
 tcctctcaag ccgcgtccccc tggaggagca ggttaggtgg aaccccccagc tattagaggt 420
 cccaccccaa actcagtttgc attacacagt caccaatcta gctgggtggc cgaaaccata 480
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctggc 540
 gctgaccaag gtgggcattgc agcaaatttttgc tgccttggga gagagactga ggaagaacta 600
 tgtggaaagac attcccttac tttcaccaac cttcaacccca caggaggtct ttattcggtc 660
 cactaacatt tttcggaatc tggagtccac ccgttgggttgc ctggctggc tttccagtg 720

tcagaaagaa ggacccatca tcatccacac tcatcagaagca gattcagaag tcttgttatcc 780
 caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
 tttacagcca ggaatctcg aggattgaa aaaggtaag gacaggatgg gcattgacag 900
 tagtgataaa gtggacttct tcatttcctt ggacaacgtg gctgccgagc aggcacacaa 960
 cctcccaagc tgccccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020
 cacatcctt tacatactgc ccaaggaaga cagggaaagt cttagatgg cagtaggccc 1080
 attcctccac atccttagaga gcaacctgct gaaagccatg gactctgcca ctgccccca 1140
 caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctttaat 1200
 gaccctgggg attttgacc acaaattggcc accgtttgct gttgacctga ccatggaact 1260
 ttaccagcac ctggaatcta aggagtggtt tgtgcagctc tattaccacg ggaaggagca 1320
 ggtgccgaga ggtgccctg atggctctg cccgctggac atgttcttga atgcccattgc 1380
 agtttataacc ttaagccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
 agttgaaat gaagagtaac tgatttataa aagcaggatg tggatttt aaaataaaagt 1500
 gccttataac aatg 1514

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

Met	Ile	Thr	Gly	Val	Phe	Ser	Met	Arg	Leu	Trp	Thr	Pro	Val	Gly	Val
1															15

Leu	Thr	Ser	Leu	Ala	Tyr	Cys	Leu	His	Gln	Arg	Arg	Val	Ala	Leu	Ala
			20						25					30	

Glu	Leu	Gln	Glu	Ala	Asp	Gly	Gln	Cys	Pro	Val	Asp	Arg	Ser	Leu	Leu
			35					40					45		

Lys	Leu	Lys	Met	Val	Gln	Val	Val	Phe	Arg	His	Gly	Ala	Arg	Ser	Pro
			50						55				60		

Leu	Lys	Pro	Leu	Pro	Leu	Glu	Glu	Gln	Val	Glu	Trp	Asn	Pro	Gln	Leu
			65						70				75		80

Leu	Glu	Val	Pro	Pro	Gln	Thr	Gln	Phe	Asp	Tyr	Thr	Val	Thr	Asn	Leu
			85						90				95		

Ala	Gly	Gly	Pro	Lys	Pro	Tyr	Ser	Pro	Tyr	Asp	Ser	Gln	Tyr	His	Glu
			100						105				110		

Thr	Thr	Leu	Lys	Gly	Gly	Met	Phe	Ala	Gly	Gln	Leu	Thr	Lys	Val	Gly
			115						120				125		

Met	Gln	Gln	Met	Phe	Ala	Leu	Gly	Glu	Arg	Leu	Arg	Lys	Asn	Tyr	Val
			130						135				140		

Glu	Asp	Ile	Pro	Phe	Leu	Ser	Pro	Thr	Phe	Asn	Pro	Gln	Glu	Val	Phe
			145						150				155		160

Ile	Arg	Ser	Thr	Asn	Ile	Phe	Arg	Asn	Leu	Glu	Ser	Thr	Arg	Cys	Leu
			165						170				175		

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His
 180 185 190
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys
 195 200 205
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
 210 215 220
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
 225 230 235 240
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
 245 250 255
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg
 260 265 270
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile
 275 280 285
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe
 290 295 300
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr
 305 310 315 320
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val
 325 330 335
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp
 340 345 350
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu
 355 360 365
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val
 370 375 380
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn
 385 390 395 400
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
 405 410 415
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
 420 425
 <210> 143
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 143
ccaactacca aagctgctgg agcc 24

<210> 144
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 144
gcagctctat taccacggga agga 24

<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 145
tccttcccggt ggtaatagag ctgc 24

<210> 146
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 146
ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg 45

<210> 147
<211> 1686
<212> DNA
<213> Homo sapiens

<400> 147
ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttcttagc 60
cttaaatttc agctcatcac cttcacctgc cttggtcatg gctctgctat tctccttgat 120
ccttgcatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtggg 180

<210> 148

<211> 347

<212> PRT

<213> *Homo sapiens*

<400> 148

Met. Ala. I.

Next And Bed Bed The Set Bed Tie Bed Mid Tie S/S T/S T/S T/S T/S

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Itp Gly Thr Val
 35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
 100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
 115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
 130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
 145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
 165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
 180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
 195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
 210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
 225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Asp Asn Leu Cys Ser Gly Arg
 245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
 260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
 275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
 290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
 305 310 315 320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
 325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 149	
ttcagctcat cacccatccc tgcc	24
<210> 150	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 150	
ggctcataaca aaataaccact aggg	24
<210> 151	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 151	
gggcctccac cgctgtgaag ggcgggtgga ggtggAACAG aaaggccagt	50
<210> 152	
<211> 1427	
<212> DNA	
<213> Homo sapiens	
<400> 152	
actgcactcg gttctatcga ttgaattccc cggggatctt ctagagatcc ctgcaccccg 60	
acccacgcgt cccggggacgc gtggggggac gcgtggggcg gctaccaggaa agagtctgcc 120	
gaaggtgaag gccatggact tcataccatc cacagccatc ctgcggctgc tggtcggtg 180	
cctggcggtc ttccggcttc tccgggtgtc gcgtgggtg cgcggaaagg cctacctgcg 240	
aatgtgtgtg gtgggtatca caggccac ctccaggctg ggcaaaaat gtgcaaaatgt 300	
tttctatgtc ggggggtgtca aactgggtctt ctgtggccgg aatgggtgggg ccctagaaga 360	
gctcatcaga gaaccttaccg cttctatgc caccaagggtt cagacacacaa agccttaactt 420	
ggtgcacccctt gacccacacag actctggggc catagtttgc gcagcagctg agatcctgc 480	
gtgtttggc tatgtcgaca tacttgtcaa caatgtgtttt atcagctacc gtgggttaccat 540	
catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggccccagt 600	
tgtcttaacg aaagcactcc tggccctccat gatcaagagg aggcaaggcc acattgtcgc 660	
catcagcagc atccaggcca agatgagcat tccttttgc tcagcatatg cagccctccaa 720	
gcacgcaccc caggctttt ttgactgtctt gctgtggccgg atggaaacagt atgaaaatgt 780	
ggtgaccgcgtc atcagcccc gctacatcca caccaacccctc tctgttaatgtt ccatcacccgc 840	
ggatggatctt aggtatggat ttatggacac caccacagcc caggggccgaa gcccctgtgaa 900	
ggtgcccccag gatgttcttgc ctgtgtgggg gaagaagaag aaagatgtga tccctggctga 960	
cttactgcct tccttggctg tttatcttcg aactctggctt cctggggctct tccctcaggct 1020	
catggccctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080	

agggccaggc cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcac 1140
 ttgtttagac tttaatggag atttgtctca caagtggaa agactgaaga aacacatctc 1200
 gtgcagatct gctggcagag gacaatcaa aacgacaaca agcttcttcc cagggtgagg 1260
 ggaaacactt aaggaataaa tatggagctg gggtaaca ctaaaaacta gaaataaaca 1320
 tctcaaacag taaaaaaaaaaa aaaaaaggc gcgcgcact ctagagtca cctgcagaag 1380
 cttggccgcc atggcccaac ttgttattg cagcttataa tggttac 1427

<210> 153
 <211> 310
 <212> PRT
 <213> Homo sapiens

<400> 153
 Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
 1 5 10 15
 Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
 20 25 30
 Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
 35 40 45
 Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
 50 55 60
 Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
 65 70 75 80
 Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
 85 90 95
 Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala
 100 105 110
 Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
 115 120 125
 Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
 130 135 140
 Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
 145 150 155 160
 Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
 165 170 175
 Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
 180 185 190
 Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
 195 200 205
 Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg 225	230	235
Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val Glu 245	250	255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val 260	265	270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu 275	280	285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu 290	295	300
Arg Lys Ser Lys Asn Ser 305	310	
<210> 154		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 154		
ggtgctaaac tggcgctctg tggc		24
<210> 155		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 155		
cagggcaaga tgagcattcc		20
<210> 156		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		

<400> 156		
tcatactgtt ccatctcgac acgc		24
<210> 157		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 157		
aatgggtggg ccctagaaga gctcatcaga gaactcacccg cttctcatgc		50
<210> 158		
<211> 1771		
<212> DNA		
<213> Homo sapiens		
<400> 158		
ccccacgcgtc cgctgggtt agatcgagca accctctaaa agcagttag agtggtaaaa 60 aaaaaaaaaa acacaccaaa cgctcgacg cacaaggatgg atgaaatttc ttctggacat 120 cctcctgctt ctcccgttac tgatcgtctg ctccctagag tcctcgtga agcttttat 180 tcctaagagg agaaaatcag tcaccggcga aatcgtgtg attacaggag ctgggcatgg 240 aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctgg 300 tataaataag catggactgg aggaaacacgc tgccaaatgc aaggactgg gtgccaaggt 360 tcatacctt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420 gaaggcagaa attggagatg tttagtatttt agtaataat gctggtagt totatacatc 480 agattgtt gctacacaag atcctcagat taaaagact tttgaagtt atgtacttgc 540 acatttctgg actacaaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600 tgtcaactgtg gttcggcag ctggacatgt ctcggcccc ttcttactgg cttactgttc 660 aagcaagttt gctgctgtt gatttcataa aactttgaca gatgaactgg ctgccttaca 720 aataactgga gtcaaaacaa catgtctgtg tcctaatttc gtaaacactg gtttcatcaa 780 aaatccaagt acaagtttg gaccactct ggaacctgag gaagtggtaa acaggctgat 840 gcatgggatt ctgactgagc agaagatgtat ttatttcca tcttctatag ctttttaac 900 aacatggaa aggatccttc ctgagcgtt cctggcagtt taaaacgaa aaatcagtgt 960 taagttgtat gcagttattt gatataaaat gaaagcgcac taagcaccta gttttctgaa 1020 aactgattta ccagggttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080 cttctgttt ttcttaattt ccccatatc tcaatatcat ttggaggct ttggcagtct 1140 tcatttacta ccactgttc tttagccaaa agctgattac atatgatata aacagagaaa 1200 tacctttaga ggtgacttta aggaaaatga agaaaaagaa cccaaatgac ttattttaaa 1260 taatttccaa gattattgt ggctcacctg aaggcttgc aaaatttgc ccataaccgt 1320 ttatttaaca tatattttt ttttgattt cacttaaatt ttgtataatt tgtgtttctt 1380 tttctgttct acataaaaatc agaaaacttca agtctctaa ataaaatgaa ggactatatc 1440 tagtgttattt tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctaccatt 1500 gccactctgt ttcctgagag atacccatc ttccaaatgcc aaacatttct gcacaggaa 1560 gcttagaggta gatacacgtt ttgcagttat aaaagcatca ctgggattta aggagaattt 1620 agagaatgta cccacaaatg gcagcaataa taaatggatc acactaaaaaaa aaaaaaaaaa 1680 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1771		
<210> 159		

<211> 300

<212> PRT

<213> Homo sapiens

<400> 159

Met	Lys	Phe	Leu	Leu	Asp	Ile	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Ile	Val
1															15

Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg	Arg	Lys
															30
20								25							

Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	His	Gly	Ile
															45
35							40								

Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	Ser	Lys	Leu	Val
															60
50							55								

Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	Thr	Ala	Ala	Lys	Cys
															80
65							70			75					

Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	Val	Val	Asp	Cys	Ser	Asn
															95
85							90								

Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	Lys	Val	Lys	Ala	Glu	Ile	Gly
															110
100							105								

Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp
															125
115							120					125			

Leu	Phe	Ala	Thr	Gln	Asp	Pro	Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn
															140
130							135								

Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
															160
145							150				155				

Lys	Asn	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His
															175
165							170								

Val	Ser	Val	Pro	Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala
															190
180							185								

Val	Gly	Phe	His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile
															205
195							200								

Thr	Gly	Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn	Phe	Val	Asn	Thr	Gly
															220
210							215								

Phe	Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly	Pro	Thr	Leu	Glu	Pro	Glu
															240
225							230				235				

Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly	Ile	Leu	Thr	Glu	Gln	Lys	Met
															255
245							250								

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
 290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 161

atccccatgca tcagcctgtt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 162

gctgggttag tctatacatc agatttgttt gctacacaag atccctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

cccacgcgtc cgccggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgccgc 60
 tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaaggta 120

attgttgc tggctctgtt gatgcctggc ccctgtgatg ggctgttcg ctccctatac 180
 agaagtgtt ccatgccacc taaggagac tcaggacagc cattattct cacccttac 240
 attgaagctg ggaagatcca aaaagaaga gaatttagtt tggtcgccc ttcccaggaa 300
 ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaacctc 360
 ttcttcgtt tcttcccaggc tcagatacag ccagaagatg ccccaactgt tctctggcta 420
 cagggtggc cgggagggttc atccatgttt ggactcttg tggacatgg gccttatgtt 480
 gtcacaagta acatgacccctt gctgtacaga gacttccctt ggaccacaac gctctccatg 540
 ctttacattt acaatccagt gggcacaggc ttcatgtttt ctgtatgatac ccacggatata 600
 gcagtcaatg aggacgatgt agcacggat ttatacagtg cactaattca gttttccag 660
 atatttcgtt aatataaaaaa taatgacttt tatgtcactg gggagtccta tgcaggaaa 720
 tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780
 aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840
 tatgcagaat tctgtacca aattggctt tggatgaga agcaaaaaaaaaa gtacttccag 900
 aagcagtgcc atgaatgcat agaacacatc aggaaggcaga actggttga ggccttggaa 960
 atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatgtt 1020
 acaggatgtt gtaattacta taacttttg cggtgcacgg aacctgagga tcaagcttac 1080
 tatgtgaaat tttgtcact cccagaggtg agacaaggcca tccacgtggg gaatcagact 1140
 ttaatgatg gaactatagt tgaaaagtac ttgcgagaag atacagtaca gtcagttaaag 1200
 ccatggtaa ctgaaatcat gaataattat aaggttctga tctacaatgg ccaactggac 1260
 atcatcggtt cagctgccct gacagagcgc tccttgatgg gcatggactg gaaaggatcc 1320
 caggaataca agaaggcaga aaaaaaaaaa ttggagatct ttaaatctga cagtgaagtg 1380
 gctggttaca tccggcaagc gggtgacttc catcaggtaa ttattcgagg tggaggacat 1440
 attttaccct atgaccagcc tctgagagct tttgacatgta ttaatcgatt catttatgg 1500
 aaaggatggg atccttatgt tggataaaact accttcccaa aagagaacat cagaggttt 1560
 cattgctgaa aagaaaaatcg taaaaacaga aaatgtcata ggaataaaaaa aattatctt 1620
 tcataatctgc aagatttttt tcatcaataa aaattatctt tgaaacaagt gagctttgt 1680
 ttttgggggg agatgtttac tacaaaatta acatgagttac atgagtaaga attacattat 1740
 ttaactaaa ggtatggaaagg tatggatgat gtgacactga gacaagatgt ataaaatgaaa 1800
 ttttagggtc ttgaatagga agtttaatt tcttctaaga gtaagtggaa agtgcagttg 1860
 taacaaacaa agtctgtaca tcttttctg ccaataacag aagtttggca tgccgtgaag 1920
 gtgtttggaa atattattgg ataagaatag ctcaattatc ccaaataaat ggtatggact 1980
 ataataatgtt tggggaaaaag attctcaat gtataaagtc ttggaaacaaa agaattctt 2040
 gaaataaaaaa tattatatat aaaagaaaaa aaaaaaa 2076

<210> 164
 <211> 476
 <212> PRT
 <213> Homo sapiens

<400> 164
 Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
 1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65	70	75	80
Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Pro Ala Gln			
85		90	95
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro			
100		105	110
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val			
115		120	125
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr			
130		135	140
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser			
145		150	155
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala			
165		170	175
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu			
180		185	190
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys			
195		200	205
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg			
210		215	220
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser			
225		230	235
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile			
245		250	255
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His			
260		265	270
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu			
275		280	285
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr			
290		295	300
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys			
305		310	315
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro			
325		330	335
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly			
340		345	350

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His
435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 165

ttccatgcc a cctaaggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 167
agctctcaga ggctggcat aggg 24

<210> 168
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 168
gtcggccctt tcccaggact gaacatgaag agttatgccg gtttcctcac 50

<210> 169
<211> 2477
<212> DNA
<213> Homo sapiens

<400> 169
cgagggcattt tccggctccg gaatggcaca tgtggaaatc ccagtcttgt tggctacaac 60
atttttccct ttccctaaca gttctaaca ctgttctaac agcttagtcat caggggttct 120
tcttgcttga gaagaaaaggc ctgaggcag acgaggcac tctcactcag ggtgaccagc 180
tccttgccctc tctgtggata acagagcatg agaaaagtcaa gagatgcagc ggagtggagg 240
gatggaaatgc taaaatagga aggaattttg ttttgcataat cagactctgg gagcagttga 300
cctggagagc ctgggggagg gcctgcctaa caagcttca aaaaacagga gcgacttcca 360
ctgggcttggg ataagacgtg ccggtaggtt agggaaagact gggtttagtc ctaatatcaa 420
attgactggc tgggtgaact tcaacagcct ttaacacctt ctgggagatg aaaacgttgg 480
cttaaggggc cagaaataga gatgcttgtt aaaaataaaat tttaaaaaaaa gcaagtattt 540
tatagcataa aggcttagaga ccaaaataga taacaggatt ccctgaacat tcctaagagg 600
gagaaatgtt gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660
accaggatgg ggaccctggg tcaggccagc ctcttgcctt ctccggaaa ttattttgg 720
tctgaccact ctgccttgc ttttgcagaa tcatgtgagg gccaaccggg gaaggtggag 780
cagatgagca cacacaggag ccgtctccctc accggccccc ctctcagcat ggaacagagg 840
cagccctggc cccggggccct ggagggtggac agccgccttg tggctctgt ctctgtggc 900
tgggtgtgc tggccccccc agcagccggc atgcctcagt tcagcacctt ccactctgag 960
aatcgtgact ggaccccttcaaa ccacttgacc gtccaccaag ggacgggggc cgtctatgt 1020
ggggccatca accgggtcta taagctgaca ggcaacctga ccattcaggt ggctcataag 1080
acagggccag aagaggacaa caagtctcgat taccggcccc tcatctgca gccctgcagc 1140
gaagtgtca ccctcaccaaa caatgtcaac aagctgtca tcattgacta ctctgagaac 1200
cgccctgtgg cctgtggag cctctaccag ggggtctgca agctgtgcg gctggatgac 1260
ctcttcatcc tggtgagcc atcccaacaa aaggagactt acctgtccag tgtcaacaag 1320
acgggcacca tgtacggggat gattgtgcgc tctgagggtt aggtggcaa gctcttcatc 1380
ggcacggctg tggatggaa gcaggattac ttcccgaccg tttccagccg gaagctgccc 1440
cgagaccctg agtccctcagc catgctcgac tatgagctac acagegattt tgtctcctct 1500
ctcatcaaga tcccttcaga caccctggcc ctggctccc actttgacat cttctacatc 1560
tacggcttg ctagtggggg ctttgcctac tttctcaactg tccagccgaa gaccctgag 1620
ggtgtggcca tcaactccgc tggagacctc ttctacaccc cacgcacatgt gcccgtctgc 1680

aaggatgacc ccaagttcca ctcatacgtg tccctgcacct tcggctgcac ccggggccggg 1740
 gtggaataacc gcctcctgca ggctgcttac ctggccaagc ctggggactc actggcccag 1800
 gccttcaata tcaccagcca ggacgatgta ctcttgccta tcttctccaa agggcagaag 1860
 cagtatcacc acccgccccga tgactctgcc ctgtgtgcct tccctatccg gcccatcaac 1920
 ttgcagatca aggagcgcct gcagtccctgc taccaggcgg agggcaacct ggagctcaac 1980
 tggctgctgg ggaaggacgt ccagtgcacg aaggcgcctg tccccatcga tgataacttc 2040
 tgtggactgg acatcaacca gcccctggga ggctcaactc cagtggaggg cctgaccctg 2100
 tacaccacca gcagggaccg catgacctct gtggcctcc acgtttacaa cggctacagc 2160
 gtggtttttg tggggactaa gagtgccaa ctgaaaaagg taagagtcta tgagttcaga 2220
 tgctccaatg ccattcacct cctcagcaaa gagtccctct tggaaaggtag ctattggtag 2280
 agatttaact ataggcaact ttatttctt ggggaacaaa ggtgaaatgg ggaggttaaga 2340
 aggggttaat ttgtgactt agcttctagc tacttcctcc agccatcagt cattgggtat 2400
 gtaaggaatg caagcgtatt tcaatatttc ccaaacttta agaaaaaaact ttaagaaggt 2460
 acatctgcaa aagcaaa 2477

<210> 170
 <211> 552
 <212> PRT
 <213> Homo sapiens

<400> 170
 Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
 1 5 10 15
 Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
 20 25 30
 Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
 35 40 45
 Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
 50 55 60
 Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
 65 70 75 80
 Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
 85 90 95
 Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
 100 105 110
 Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
 115 120 125
 Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
 130 135 140
 Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
 145 150 155 160
 Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
 165 170 175

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
 180 185 190

Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
 195 200 205

Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
 210 215 220

Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
 225 230 235 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
 245 250 255

Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
 260 265 270

Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
 275 280 285

Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
 290 295 300

Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
 305 310 315 320

Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg
 325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe
 340 345 350

Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr
 355 360 365

Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser
 370 375 380

Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr
 385 390 395 400

His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
 405 410 415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
 420 425 430

Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
 435 440 445

Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

100

450 455 460
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr
465 470 475 480
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly
485 490 495
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val
500 505 510
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys
515 520 525
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln
530 535 540
Leu Tyr Phe Leu Gly Glu Gln Arg
545 550

<210> 171
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 171
.tggaaataccg cctcctgcag 20

<210> 172
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 172
cttctgccct ttggagaaga tggc 24

<210> 173
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

TOMTXX-0002000600

<400> 173
 ggactcactg gcccaggcct tcaatatcac cagccaggac gat 42
 <210> 174
 <211> 3106
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> modified_base
 <222> (1683)
 <223> a, t, c or g
 <400> 174
 aggctccgc gcgccgtga gtgcggactg gagtggaaac ccgggtcccc gcgccttagag 60
 aacacgcgt gaccacgtgg agcctccggc ggaggccgc ccgcacgcgt ggactcctgc 120
 tgctggtcgt ctgggcttc ctgggtgtcc gcaggcgtgaa ctggagcacc ctggtcctc 180
 tgcggctccg ccatcgacag ctggggctgc aggccaaggg ctggaacttc atgctggagg 240
 attccaccc ttggatcttc ggggctcca tccactattt ccgtgtgccc agggagtact 300
 ggagggaccg cctgctgaag atgaaggcct gtggcttcaa caccctcacc acctatgttc 360
 cgtggAACCT gcatgagcca gaaagaggca aatttgactt ctctggaaac ctggacctgg 420
 aggccttcgt cctgtatggcc gcagagatcg ggctgtgggt gattctggtt ccaggcccct 480
 acatctgcag tgagatggac ctgggggtt tgcccaagctg gctactccaa gaccctggca 540
 tgaggcttag gacaacttac aagggttca ccgaagcgt ggacccctt tttgaccacc 600
 ttagtgtccag ggtggtgcca ctccagtaca agcgtgggg acctatcatt gccgtgcagg 660
 tggagaatga atatggttcc tataataaaag acccccgcata catgccctac gtcaagaagg 720
 cactggagga ccgtggcatt gtggactgc tcctgacttc agacaacaag gatgggctga 780
 gcaaggggat tggccaggaa gtcttggca ccatcaactt gcagtcacca cacgagctgc 840
 agctactgac cacctttctc ttcaacgtcc aggggactca gcccagatg gtatggagt 900
 actggacggg gtggtttgac tggggggag gcccctcaca tatcttggat tcttctgagg 960
 ttttggaaaac cgtgtctgc attgtggacg ccggctccctc catcaacctc tacatgttcc 1020
 acggaggcac caactttggc ttcatgaatg gagccatgca ctccatgac tacaagtca 1080
 atgtcaccag ctatgactat gatgctgtgc tgacagaagc cggcgattac acggccaagt 1140
 acatgaagct tggagacttc ttggctccca tctcaggcat ccctctccct cccccacctg 1200
 accttcttcc caagatgccg tatgagccct taacgcccgt ctgtacctg tctctgtgg 1260
 acggccctcaa gtacctgggg gagccaatca agtctgaaaa gcccataac atggagaacc 1320
 tgccagtcaa tggggggaaat ggacagtcct tgggtatcat tctctatgag accagcatca 1380
 cctcgtctgg catcctcagt ggccacgtgc atgatgggg gcagggtttt gtgaacacag 1440
 tatccatagg attcttggac tacaagacaa cgaagattgc tggcccccgt atccagggtt 1500
 acaccgtgt gaggatctt gttggaaatc gtggggcgagt caactatggg gagaatattg 1560
 atgaccagcg caaaggctta attggaaatc tctatctgaa tgattcaccctt ctggaaaaact 1620
 tcagaatcta tagcctggat atgaagaaga gcttcttca gaggttccgc ctggacaaat 1680
 ggnngttccct cccagaaaca cccacattac ctgctttctt ctgggttagc ttgtccatca 1740
 gctccacgcc ttgtgacacc ttctgttgc tggggggctg ggagaagggg gttgtattca 1800
 tcaatggcca gaaccttggc cggtactggc acattggacc ccagaagacg cttaacccctt 1860
 caggtccctg gtggagcagg ggaatcaacc aggtcatgtt ttttggggag acgtggccgg 1920
 gcccctgcatt acagttcactg gaaacccccc acctggccag gaaccaggatc attaagttag 1980
 cggtggcacc ccctccctgtt ggtgcactgt ggagactgccc gcctccctt gacctgaacg 2040
 ctgggtggctg ctggcccccacc cctcactgca aaagcatctc cttaagttagc aacccctcagg 2100
 actgggggtt acagtctgcctt ctgtctcgtt ctcacccatcc taaggctgca gggaaagggtg 2160
 ggtatggctt gggccttggct ttgttgcgtt tggctttctt acagccctgc tcttgcgtcc 2220
 aggctgtcggtt gctgtctcta ggggtggggagc agctaattcgt atcgcccccctt 2280

```

cagaaaaaaagt gctgaaaacgt gcccttgcac cggacgtcac agccctgcga gcatctgcgt 2340
gactcaggcg tgctcttgc tggttcctgg gaggcgtggc cacatccctc atggccccat 2400
tttatccccg aaatcctggg tgtgtcacca gtgttagaggg tggggaaaggg gtgtctcacc 2460
tgagctgact ttgttcttcc ttccacaacct tctgagcctt ctggggatt ctggaaggaa 2520
ctcggcgtga gaaacatgtg acttcccctt tccctccca ctgcgtgtt cccacagggt 2580
gacaggctgg gctggagaaa cagaaaatcct caccctgcgt ctcccaagt tagcagggtt 2640
ctctgggtt cagtgaggag gacatgtgag tcctggcaga agccatggcc catgtctgca 2700
catccaggga ggaggacaga aggcccagct cacatgtgag tcctggcaga agccatggcc 2760
catgtctgca catccaggga ggaggacaga aggcccagct cacatgtgag tcctggcaga 2820
agccatggcc catgtctgca catccaggga ggaggacaga aggcccagct cacatgtgag 2880
tcctggcaga agccatggcc catgtctgca catccaggga ggaggacaga aggcccagct 2940
cagtggccccc cgctcccccac ccccccacgcc cgaacagcag gggcagagca gccatccctc 3000
gaagtgtgtc caagtccgca tttgagcctt gttctgggg ccagcccaac acctggctt 3060
ggctcaactgt cctgagttgc agtaaaagcta taaccttcaa tcacaa 3106

```

<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD RES

<222> (539)

<223> Any amino acid

<400> 175

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
 1 5 10 15

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
20 25 30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
35 40 45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
50 55 60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
 65 70 75 80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
 85 90 95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
100 105 110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
115 120 125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
130 135 140

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
 145 150 155 160

Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp
 165 170 175

His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
 180 185 190

Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
 195 200 205

Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
 210 215 220

Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
 225 230 235 240

Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
 .. 245 250 255

Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
 260 265 270

Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
 275 280 285

Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
 290 295 300

Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
 305 310 315 320

Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys
 325 330 335

Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly
 340 345 350

Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile
 355 360 365

Ser Gly Ile Pro Leu Pro Pro Pro Asp Leu Leu Pro Lys Met Pro
 370 375 380

Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu
 385 390 395 400

Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu
 405 410 415

Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His
 435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp
 450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val
 465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn
 485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp
 500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser
 515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr
 530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr
 545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
 565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln
 580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln
 595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
 610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
 625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

ggggacgcgg agctgagagg ctccgggcta gctagggtga ggggtggacg ggtcccagga 60
 ccctggtag ggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120
 aaggggagca aagccgggct cggcccgagg cccccaggac ctccatctcc caatgttgg 180
 ggaatccgac acgtgacggt ctgtccgccc tctcagacta gaggagcgct gtaaacgcca 240
 tggctcccaa gaagctgtcc tgccttcgtt ccctgctgct gccgctcagc ctgacgctac 300
 tgctgccccca ggcagacact cggtcgttcg tagtggatag gggcatgac cggtttctcc 360
 tagacggggc cccgttccgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

tgctttggc cgaccggctt ttgaagatgc gatggagcggtt cctcaacgcc atacagtttt 480
 atgtccctg gaactaccac gagccacacgc ctggggctta taactttaat ggcagccggg 540
 acctcattgc ctttctgaat gaggcagtc tagcgaacctt gttggtcata ctgagaccag 600
 gaccttacat ctgtcagag tgggagatgg ggggtctccc atcctggtttgc cttcgaaaac 660
 ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctggttca 720
 aggtcttgtt gccaaagata tatccatggc ttatcacaa tggggcaac atcatttagca 780
 ttcaggttga gaatgaatat ggttagtaca gagcctgtga cttcagctac atgaggcact 840
 tggctggctt ctccgtgca ctgttaggg aaaagatctt gctcttcacc acagatggc 900
 ctgaaggact caagtgtggc tccctccggg gactctatac cactgttagat tttggcccg 960
 ctgacaacat gaccaaaatc tttaccctgc ttcggaagta tgaacccat gggccattgg 1020
 taaactctga gtactacaca ggctggctgg attactgggg ccagaatcac tccacacgtt 1080
 ctgtgtcagc tptaacccaaa ggactagaga acatgctcaa gttggagcc agtgtgaaca 1140
 tgtacatgtt ccattggaggat accaactttt gatattggaa tgggtggcat aagaaggac 1200
 gtttccttcc gattactacc agctatgact atgatgcacc tatatctgaa gcaggggacc 1260
 ccacacctaa gtttttgctt ctccgagatg tcattcagcaa gttccaggaa gttcccttgg 1320
 gaccttacc tccccggc cccaagatga tgcttgacc tgcgtactctg cacctggttg 1380
 ggcatttact ggcttcctta gacttgctt gccccgtgg gcccattcat tcaatcttgc 1440
 caatgacctt tgaggctgtc aagcaggacc atggcttcat gttgtaccga accttatatga 1500
 cccataccat ttttggccca acaccattctt ggggtgccaaa taatggagtc catgaccgtt 1560
 cctatgtat ggtggatggg gtgttccagg gtgttggaa gcgaaatatg agagacaaac 1620
 tattttgac gggaaaactg gggtccaaac tggatatctt ggtggagaac atggggaggc 1680
 tcagcttgg gtctaacacgc agtgaattca agggcctgtt gaagccacca attctggggc 1740
 aaacaatctt taccctgtgg atgatgttcc ctctgaaaat tgataacctt gtgaagtgg 1800
 ggtttccctt ccattgtccca aaatggccat atcctcaagc tccttctggc cccacattct 1860
 actccaaaac atttccaaattt ttaggctcg ttggggacac atttctatat ctacctggat 1920
 ggaccaaggg ccaagtctgg atcaatgggt ttaacttggg ccgtactgg acaaagcagg 1980
 ggccacaaca gaccctctac gtgccaagat tccctgtgtt tccttaggggaa gccctcaaca 2040
 aaattacatt gctggacta gaagatgtac ctctccagcc ccaagtccaa tttttggata 2100
 agcctatcctt caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160
 atacactgag tgctctgaa ccaatggagt taagtggca ctgaaaggta gcggggcat 2220
 ggtggctcat gcctgtatcc ccagcactt gggaggctga gacgggtggaa ttacctgagg 2280
 tcaggacttcc aagaccagcc tggccaaat ggtggaaacc cgtctccactt aaaaatacaa 2340
 aaatttagccg ggcgtatgg tgggcaccc tcataccccc tacttgggag gctgagggca 2400
 ggagaatttgc ttgaatccag gaggcagagg ttgcagttagt tggaggttgc accactgcac 2460
 tccagctgg ctgacagtga gacactccat ctcaaaaaaaa aaaaaa 2505

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met	Ala	Pro	Lys	Lys	Lys	Leu	Ser	Cys	Leu	Arg	Ser	Leu	Leu	Leu	Pro	Leu
1															15	

Ser	Leu	Thr	Leu	Leu	Leu	Pro	Gln	Ala	Asp	Thr	Arg	Ser	Phe	Val	Val	
														20	25	30

Asp	Arg	Gly	His	Asp	Arg	Phe	Leu	Leu	Asp	Gly	Ala	Pro	Phe	Arg	Tyr	
														35	40	45

Val	Ser	Gly	Ser	Leu	His	Tyr	Phe	Arg	Val	Pro	Arg	Val	Leu	Trp	Ala	
														50	55	60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe
 65 70 75 80

Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe
 85 90 95

Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala
 100 105 110

Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp
 115 120 125

Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His
 130 135 140

Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe
 145 150 155 160

Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly
 165 170 175

Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala
 180 185 190

Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu
 195 200 205

Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu
 210 215 220

Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro
 225 230 235 240

Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro
 245 250 255

His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr
 260 265 270

Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly
 275 280 285

Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe
 290 295 300

His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly
 305 310 315 320

Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser
 325 330 335

Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

340	345	350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro		
355	360	365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu		
370	375	380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu		
385	390	395
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		
405	410	415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		
420	425	430
Pro Asn Asn Gly Val Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		
435	440	445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		
450	455	460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		
465	470	475
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		
485	490	495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		
500	505	510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		
515	520	525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		
530	535	540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		
545	550	555
560		
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		
565	570	575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		
580	585	590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		
595	600	605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		
610	615	620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
 645 650

<210> 178
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 178
tggctactcc aagaccctgg catg 24

<210> 179
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 179
tggacaaaatc cccttgctca gccc 24

<210> 180
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 180
gggcttcacc gaagcagtgg acctttattt tgaccacctg atgtccaggg 50

<210> 181
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 181
ccagctatga ctatgatgca cc 22

```

<210> 182
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 182
tggcacccag aatggtggtt gctc 24

<210> 183
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 183
cgagatgtca tcagcaagtt ccaggaagtt cctttgggac cttaacctcc 50

<210> 184
<211> 1947
<212> DNA
<213> Homo sapiens

<400> 184
gcttgaaca cgctcgcaag cccaaagtgc agcatctgat tggttatgag gtatttgagt 60
gcaccaccaa tatggcttac atgttgaaaa agcttctcat cagttacata tccatttattt 120
gtgttatgg ctatctgc ctctacactc tottctgggtt attcaggata cctttgaagg 180
aatattctt cggaaaagtc agagaagaga goagtttttag tgacattcca gatgtcaaaa 240
acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300
ttggtgtgtt cttgtcagaa gttagtggaaa ataaaacttag ggaaatttagt ttgaaccatg 360
agtggacatt tgaaaaactc aggccgcaca tttcacgcaa cgcccaggac aagcaggagt 420
tgcatctgtt catgtgtcg ggggtgccccg atgctgtctt tgacattcaca gacctggatg 480
tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540
acctccaaga gctccacctc tgccactgccc ctgcaaaaagt tgaacagact gcttttagct 600
ttcttcgcga tcacttgaga tgccttcacg tgaagttcac tgatgtggct gaaattcctg 660
cctgggtgtt tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720
aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780
acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840
caaagtttagt cattcataat gacggcacta aactcttggt actgaacagc cttaaagaaaa 900
tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960
ttttcagcct ctctaatttca caggaactgg atttaaagtc caataacatt cgcacaatttgc 1020
agggaaatcat cagtttccag cattaaaac gactgacttg tttaaaatttca tggcataaca 1080
aaatttgtac tattcctccc tctattaccc atgtcaaaaa cttggagtca ctttatttctt 1140
ctaaacaacaa gctcgaaatcc ttaccagtgg cagtttttag tttacagaaaa ctcagatgtct 1200
tagatgtgag ctacaacaac atttcaatga ttccaataga aataggatttgc cttcagaacc 1260
tgcagcattt gcatatcact gggaaacaaag tggacattctt gccaaacaa ttgttttaat 1320

```

gcataaaagtt gaggactttg aatctggac agaactgcat cacctcactc ccagagaaaag 1380
 ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttgc gaccgcctgc 1440
 cagcccagct gggccagtgt cgatgctca agaaaagcgg gcttgttgc gaagatcacc 1500
 ttttgatac cctgccactc gaagtcaaag aggattgaa tcaagacata aatattccct 1560
 ttgcaaatgg gatttaaact aagataatat atgcacagtg atgtgcagga acaacttcct 1620
 agattgcaag tgctcacgtt caagttttaa caagataatg catttttagga gtagatacat 1680
 cttttaaat aaaacagaga ggtatgcata gaggctgata gaagacataa ctgaatgttc 1740
 aatgttgta gggttttaag tcatttcattt ccaaattttt ttttttttcc ttttgggaa 1800
 agggaaaggaa aaattataat cactaatctt gttttttt aaattgtttg taacttggat 1860
 gctgccgcta ctgaatgtt acaaatttgc tgcctgctaa agtaaatgtat taaattgaca 1920
 ttttcttact aaaaaaaaaaaaaaaa 1947

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

Met	Ala	Tyr	Met	Leu	Lys	Lys	Leu	Leu	Ile	Ser	Tyr	Ile	Ser	Ile	Ile
1				5					10					15	

Cys	Val	Tyr	Gly	Phe	Ile	Cys	Leu	Tyr	Thr	Leu	Phe	Trp	Leu	Phe	Arg
					20			25					30		

Ile	Pro	Leu	Lys	Glu	Tyr	Ser	Phe	Glu	Lys	Val	Arg	Glu	Glu	Ser	Ser
					35			40				45			

Phe	Ser	Asp	Ile	Pro	Asp	Val	Lys	Asn	Asp	Phe	Ala	Phe	Leu	Leu	His
					50			55				60			

Met	Val	Asp	Gln	Tyr	Asp	Gln	Leu	Tyr	Ser	Lys	Arg	Phe	Gly	Val	Phe
65					70				75				80		

Leu	Ser	Glu	Val	Ser	Glu	Asn	Lys	Leu	Arg	Glu	Ile	Ser	Leu	Asn	His
					85				90				95		

Glu	Trp	Thr	Phe	Glu	Lys	Leu	Arg	Gln	Ile	Ser	Arg	Asn	Ala	Gln	
					100			105				110			

Asp	Lys	Gln	Glu	Leu	His	Ile	Phe	Met	Leu	Ser	Gly	Val	Pro	Asp	Ala
					115			120				125			

Val	Phe	Asp	Leu	Thr	Asp	Leu	Asp	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro
					130			135				140			

Glu	Ala	Lys	Ile	Pro	Ala	Lys	Ile	Ser	Gln	Met	Thr	Asn	Leu	Gln	Glu
145					150				155			160			

Leu	His	Leu	Cys	His	Cys	Pro	Ala	Lys	Val	Glu	Gln	Thr	Ala	Phe	Ser
					165				170			175			

Phe	Leu	Arg	Asp	His	Leu	Arg	Cys	Leu	His	Val	Lys	Phe	Thr	Asp	Val
					180			185				190			

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu
 195 200 205

Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu
 210 215 220

Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
 225 230 235 240

Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu
 245 250 255

Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn
 260 265 270

Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys
 275 280 285

Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln
 290 295 300

Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile
 305 310 315 320

Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn
 325 330 335

Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu
 340 345 350

Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val
 355 360 365

Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile
 370 375 380

Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu
 385 390 395 400

His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys
 405 410 415

Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser
 420 425 430

Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
 435 440 445

Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
 450 455 460

Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465	470	475	480
-----	-----	-----	-----

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro			
	485	490	495

Phe Ala Asn Gly Ile			
	500		

<210> 186

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 186

cctccctcta ttacccatgt c

21

<210> 187

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 187

gaccaacttt ctctggaggt gagg

24

<210> 188

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 188

gtcactttat ttctctaaca acaagctcga atccttacca gtggcag

47

<210> 189

<211> 2917

<212> DNA

<213> Homo sapiens

<400> 189

ccccacgcgtc cgcccttctc tctggacttt gcattttcat tcctttcat tgacaaaactg 60
actttttta tttttttt tccatctctg ggccagcttg ggatcctagg cccgcctggg 120
aagacatttg tgtttacac acataaggat ctgtgtttgg ggtttcttct tcctcccctg 180

acatggccat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgct 240
gcaccttatct gccttaggtac atcgaagtct ttgcacccctc atacagtat tatgcctgtc 300
atcgctgggt gatatcctggc ggccttgcctc ctgtctgatag ttgtctgtct ctgtctttac 360
ttcaaaaatac aacaacgcgcct aaaagctgca aaggAACCTG aagctgtggc tgtaaaaaat 420
cacaaccagg acaaggtgtg gtggccaag aacagccagg cccaaaccat tgccacggag 480
tcttgtctg ccctgcagtg ctgtgaagga tatagaatgt gtgccagtt tgattccctg 540
ccaccttgct gttgcgacat aaatgaggcct ctctgagttt gggaaaggctc cttctcaaa 600
gcagagccct gaagacttca atgatgtcaa tgaggccacc tggttgtat gtgcaggcac 660
agaagaaagg cacagctccc catcaggttc atggaaaata actcaigtgcc tgctgggaac 720
cagctgctgg agatccctac agagagttc cactggggc aacccttcca ggaaggagtt 780
ggggagagag aaccctcaact gtggggatag ctgataaacc agtcacacag ctgctctatt 840
ctcacacaaa tctaccctt gctggctgg aactgacgtt tccctggagg tgcagaaaa 900
gctgatgtaa cacagagcct ataaaagctg teggtcctta aggctgccc ggccttgcc 960
aaaatggagc ttgtaagaag gctcatgcca ttgaccctct taattctctc ctgtttggcg 1020
qagctgacaa tggcgaggc tgaaggcaat gcaagctgca cagtcagttt aggggggtgcc 1080
aatatggcag agacccacaa agccatgatc ctgcaactca atcccagtga gaactgcacc 1140
tggacaatag aaagaccaga aaacaaaagc atcagaattt tctttccta tgcagggat 1200
gatccagatg gaagctgtga aagtggaaac ataaaagtct ttgacggAAC ctccagcaat 1260
gggcctctgc tagggcaagt ctgcagttt aacgactatg ttccctgtatt tgaatcatca 1320
tccagttacat tgacgtttca aatagttact gactcagcaa gaattcaaag aactgtctt 1380
gttctctact acttcttctc tcctaacatc totattccaa actgtggcggtt accttgat 1440
accttggaaag gatccttacac cagccccat tacccaaagc cgcatcctga gctggcttat 1500
tgcgtgtggc acatacaagt ggagaagat tacaagataa aactaaactt caaagagatt 1560
ttccctagaaa tagacaaaca gtcaaaattt gatTTTCTTG ccatctatga tggcccttcc 1620
accaactctg gcctgattgg acaagtcgtt ggcctgtga ctcccaccc tgaatcgca 1680
tcaaaactctc tgactgtcgt gttgtotaca gattatgcca attcttaccg gggattttct 1740
gcttcctaca cctcaattt tgcagaaaaac atcaacacta catcttaac ttgcctttct 1800
gacaggatga gagtttattt aagcaaatcc taccttaggg cttttaactc taatggaaat 1860
aacttgcacac taaaagaccc aacttgcaga cccaaattat caaatgtgtt ggaattttct 1920
gtccctctta atggatgtgg tacaatcaga aaggtagaag atcagtcaat tacttacacc 1980
aatataatca cctttctgc atcctcaact totgaagtga tcaccgtca gaaacaactc 2040
cagattattt tgaagtgtga aatggacat aattctacag tggagataat atacataaca 2100
qaagatgtatg taatacaag tcaaaatgca ctggggcaaat ataacaccag catggcttt 2160
tttgaatcca attcatttga aaagactata ctgtaatcac catattatgt ggatttgaac 2220
caaactcttt ttgttcaagt tagtctgcac acctcagatc caaatttggg ggtgtttctt 2280
gatacctgtt gaggcctctcc cacctctgac ttgcacccctt caacctacga ctaatcaag 2340
agtggatgtt gtcgagatga aacttgcata gttgtatccctt tattttggaca ctatgggaga 2400
ttcccttttta atgcctttaa attcttggaa agatgcgtt ctgtgtatctt gcaatgtaa 2460
gttttgcataat gtcgatgcgt tgaccacccat tccgcgtgc atcaaggatgg tgcctccaga 2520
agcaaaacgg acaatttcttca atataaatgg aaaaacagattt ccatcatagg acccattcgt 2580
ctgaaaaggg atcgaagtgc aagtggcaat tcaggatttc agcatgaaac acatgcggaa 2640
gaaactccaa accagccctt caacagtgtg catctgtttt ccttcatggt tctagctctg 2700
aatgtgggtt gtcgatgcgt aatcacaatgtt aggcatgggg taaatcaacg ggcagactac 2760
aaataccaga agctgcagaa ctattaacta acagggtccaa ccctaagtga gacatgtttc 2820
tccaggatgc caaaggaaat gctacatgtt ggctacacat attatgaata aatgagggaa 2880
ggcctgaaaat tgacacacag gctgcgtatgt aaaaaaaaaa 2917

<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser
 1 5 10 15

Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys
 20 25 30

Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met
 35 40 45

Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
 50 55 60

Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp
 65 70 75 80

Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr
 85 90 95

Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr
 100 105 110

Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val
 115 120 125

Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe
 130 135 140

Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr
 145 150 155 160

Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu
 165 170 175

Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile
 180 185 190

Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys
 195 200 205

Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu
 210 215 220

Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser
 225 230 235 240

Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg
 245 250 255

Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr
 260 265 270

Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys
 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys
 290 295 300
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val
 305 310 315 320
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile
 325 330 335
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val
 340 345 350
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly
 355 360 365
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile
 370 375 380
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe
 385 390 395 400
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val
 405 410 415
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp
 420 425 430
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser
 435 440 445
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg
 450 455 460
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe
 465 470 475 480
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu
 485 490 495
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys
 500 505 510
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys
 515 520 525
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg
 530 535 540
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu
 545 550 555 560
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

565	570	575
Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe 580 585 590		
Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr 595 600 605		
<210> 191		
<211> 21		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 191		
tctctattcc aaactgtggc g		21
<210> 192		
<211> 22		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 192		
tttgatgacg attcgaagg t		22
<210> 193		
<211> 47		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 193		
ggaaggatcc ttaccagcc ccaattaccc aaagccgcatttgc		47
<210> 194		
<211> 2362		
<212> DNA		
<213> Homo sapiens		
<400> 194		
gacggaaagaa cagcgctccc gagggccgcgg gagcctgcag agaggacagc cggcctgcgc 60		
cgggacatgc ggccccagg gctccccagg ctcgcgttcc cggtgtgtgttgc 120		
ctgctgtgc cggccgcggcc gtgcctgcc cacagcgcca cgcgcgttgcga cccccacctgg 180		

gagtcctgg acgcccggca gctgcccgcg tggttttagcc aggccaagtt cggcatcttc 240
 atccactggg gagtgtttc cgtgcccagc ttccggtagcg agtggttctg gtggatttgg 300
 caaaaaggaaa agataccgaa gtatgtggaa ttatgaaag ataattaccc tcctagttc 360
 aaatatgaag attttggacc actattaca gcaaaaatttt ttaatgcca ccagtggca 420
 gatattttc aggccctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480
 ttacccgtt ggggtcaga atattcgtgg aactggaaatg ccatagatga ggggccccaaag 540
 agggacattg tcaaggaact tgaggttagcc attagaaca gaactgaccc gcgttttgg 600
 ctgtactatt cccttttga atggtttcat ccgtcttcc ttgaggatga atccagttca 660
 ttccataaggc ggaatttcc agtttctaag acattgcccag agctctatga gttagtgaac 720
 aactatcagc ctgaggttct gtggctggat ggtgacggag gggccggca tcaatactgg 780
 aacagcacag gtttcttggc ctgggtatataatgaaagcc cagttcccccc cacagtagtc 840
 accaatgatc gttggggagc tgtagcatc tgtaagcatg gtggcttcta tacctgcagt 900
 gatcgttata acccaggaca tcttttgcataaaatggg aaaactgcata gacaatagac 960
 aaactgtcct ggggctatag gaggaaatg ggaatctctg actatcttac aattgaagaa 1020
 ttgggtgaagc aacttgtaga gacagttca tggggaggaa atctttgtat gaatatttggg 1080
 cccacactag atggcaccat ttctgttagtt ttggggaggc gactgaggca agtggggtcc 1140
 tggctaaaag tcaatggaga agctatttat gaaacctata cctggcgatc ccagaatgac 1200
 actgtcacc cagatgtgtg gtacacatcc aagcctaaag aaaaattagt ctatgccatt 1260
 ttctttaat gccccacatc aggacagctg ttcccttggcc atcccaaagc tattctgggg 1320
 gcaacagagg tgaaactact gggccatggc cagccactta actggatttc ttggagcaa 1380
 aatggcatta tggtagaact gccacagcta accattcatc agatggcgatc taaatggggc 1440
 tgggctctag ccctaactaa tgtgatctaa agtgcagcgag agtggctgat gctgcaagtt 1500
 atgtcttaagg ctaggaacta tcaggtgtct ataattgttag cacatggaga aagcaatgta 1560
 aactggataa gaaaattatt tggcagttca gccccttcccc tttttccac taaatttttc 1620
 ttaaattacc catgtAACCA ttttaactct ccagtgcact ttgcattaa agtctttca 1680
 cattgatttgc ttccatgtg tgactcagag gtggaaattt tttcacatta tagtagcaag 1740
 gaattggggg tattatggac cgaactgaaa attttatgtt gaagccatata ccccatgat 1800
 tatatagtta tgcatcaattt aatatggggat tattttctgg gaaatgcatt gctgtcaat 1860
 tttttttgt gccaacatca tagagtgtat ttacaaaatc ctagatggca tagcctacta 1920
 cacacctaattt gtgtatggta tagactgttgc ttccctaggctt acagacatata acagcatgtt 1980
 actgaataactt gtggcaata gtaacagtgat tattttgtata tcgaaacata tggaaacata 2040
 gagaaggtaa agtaaaaata ctgtaaaata aatgggtgcac ctgtataggc cacttaccac 2100
 gaatggagct tacaggactg gaagttgtc tgggtgagtc agtgagtgaa tgtgaaggcc 2160
 taggacatta ttgaacactg ccagacgtttaaaatctgtt atgcttaggc tacactacat 2220
 ttataaaaaa aagtttttctt ttcttcaattt ataaattaac ataaatgtac tgtaacttta 2280
 caaacgtttt aattttaaa accttttgg ctcttttgcataaacttta gcttaaaaaca 2340
 taaactcattt gtgcaaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu

1

5

10

15

Leu Leu Leu Leu Pro Pro Pro Cys Pro Ala His Ser Ala Thr

20

25

30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala

35

40

45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
 50 55 60

Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
 65 70 75 80

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro
 85 90 95

Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe
 100 105 110

Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr
 115 120 125

Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser
 130 135 140

Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp
 145 150 155 160

Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg
 165 170 175

Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu
 180 185 190

Glu Asp Glu Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys
 195 200 205

Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val
 210 215 220

Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser
 225 230 235 240

Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr
 245 250 255

Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly
 260 265 270

Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro
 275 280 285

His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr
 290 295 300

Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val
 305 310 315 320

Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
 450 455 460

Asn Val Ile
 465

<210> 196
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 196
tggtttgacc aggccaagtt cggtt 23

<210> 197
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 197
ggattcatcc tcaaggaaga gcgg 24

<210> 198

<211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 198
 aacttgcagc atcagccact ctgc 24

<210> 199
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 199
 ttccgtgccc agcttcggta gcgagtggtt ctgggtggat tggca 45

<210> 200
 <211> 2372
 <212> DNA
 <213> Homo sapiens

 <400> 200
 agcaggaaaa tcggatgtc tcggttatga agtggagcag tgagtgttag cctcaacata 60
 gttccagaac ttcctatccg gactagttat tgagcatctg cctctcatat caccagtggc 120
 catctgagggt gttccctgg ctctgaagggt gttaggcacga tggccagggtg cttcagccctg 180
 gtgttgccttc tcaactccat ctggaccacg aggctcctgg tccaaggctc tttgcgtgca 240
 gaagagctt ccattccagggt gtcatgcaga attatggggta tcacccttgt gagcaaaaag 300
 gcgaaccacgc agctgaattt cacagaagct aaggaggcct gttagctgct gggactaagt 360
 ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420
 ggctgggttg gagatggatt cgtggtcattc tctaggattt gcccaaacc 480
 aaaaatgggg tgggtgcctt gatttggaa gttccagtga gccgacagtt tgcagccatat 540
 tgttacaact catctgatac ttggactaac tcgtgcattc cagaaaattat caccaccaaa 600
 gatccccatata tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcac 660
 acctactcggtt tggcatcccc ttactctaca atacctgccctt ctactactac tccctcctgt 720
 ccagcttcca cttctattcc acggagaaaa aaatttgattt gtgtcacaga agtttttatg 780
 gaaactagca ccattgtctac agaaactgaa ccattgttg aaaataaaagc agcattcaag 840
 aatgaagctg ctgggtttgg aggtgtcccc acggctctgc tagtgcttgc tctcctcttc 900
 tttgggtctg cagctggctt tggattttgc tatgtcaaaa ggtatgtgaa ggccttcctt 960
 ttacaaaca agaatcagca gaaggaaaatg atcgaaacca aagttagtaaa ggaggagaag 1020
 gccaatgata gcaaccctaa tgaggaatca aagaaaaactg ataaaaaacc 1080
 aagagtccaa gcaaaaactac cgtgcgtgc ctggaaagctg aagtttagat gagacagaaaa 1140
 tgaggagaca cacctgaggc tggtttctt catgctcattt accctgcccc agctggggaa 1200
 atcaaaaaggc ccaaagaacc aaagaagaaa gtccaccctt ggttcctaacc tggaaatcagc 1260
 tcaggactgc cattggacta tggagtgcac caaagagaat gcccttcctt ttattgtaac 1320
 cctgtctgga tcctatccctc ctaccccaa agctcccac ggccttcta gcctggctat 1380
 gtcctaataa tatcccactg ggagaaagga gtttgcaaaa gtgcaaggac ctaaaaacatc 1440

tcatcagtat ccagtggtaa aaaggcctcc tggctgtctg aggctaggtg gtttggaaagc 1500
 caaggagtca ctgagaccaa ggctttctt actgattccg cagctcagac cctttcttca 1560
 gctctgaaag agaaacacgt atccccacctg acatgtcctt ctgagcccg taagagcaaa 1620
 agaatggcag aaaagtttag cccctgaaag ccatggagat tctcataact tgagacctaa 1680
 tctctgtaaa gctaaaataa agaaatagaa caaggctgag gatacagacag tacactgtca 1740
 gcagggactg taaacacaga cagggtcaaa gtgtttctt tgaacacatt gagttggat 1800
 cactgtttag aacacacaca cttactttt ctggctctta ccactgctga tattttctt 1860
 agaaaaataa ctttacaag taacaaaaat aaaaactctt ataaatttctt atttttatct 1920
 gagttacaga aatgattact aaggaagatt actcagtaat ttgtttaaaa agtaataaaa 1980
 ttcaacaaac atttgctgaa tagtactat atgtcaagtgt ctgtgcagg tattacactc 2040
 tgtaattgaa tattattcct caaaaaattt cacatagtag aacgctatct gggaaagctat 2100
 tttttcagt tttgatattt cttagttatc tacttccaaa ctaatttttta ttttgctga 2160
 gactaatctt attcattttc tctaataatgg caaccattat aacctaattt tattattaac 2220
 atacctaaga agtacattgt taccttata taccaaagca cattttaaaa gtgccattaa 2280
 caaatgtatc actagccctc cttttccaa caagaaggaa ctgagagatg cagaaatatt 2340
 tgtgacaaaaa aattaaagca ttttagaaaaac tt 2372

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

Met	Ala	Arg	Cys	Phe	Ser	Leu	Val	Leu	Leu	Leu	Thr	Ser	Ile	Trp	Thr
1															15

Thr	Arg	Leu	Leu	Val	Gln	Gly	Ser	Leu	Arg	Ala	Glu	Glu	Leu	Ser	Ile
20								25							30

Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	Ile	Thr	Leu	Val	Ser	Lys	Lys	Ala
35								40					45		

Asn	Gln	Gln	Leu	Asn	Phe	Thr	Glu	Ala	Lys	Glu	Ala	Cys	Arg	Leu	Leu
50								55					60		

Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu	Thr	Ala	Leu	Lys	Ala
65								70					75		80

Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val	Gly	Asp	Gly	Phe	Val	Val
85								90					95		

Ile	Ser	Arg	Ile	Ser	Pro	Asn	Pro	Lys	Cys	Gly	Lys	Asn	Gly	Val	Gly
100								105					110		

Val	Leu	Ile	Trp	Lys	Val	Pro	Val	Ser	Arg	Gln	Phe	Ala	Ala	Tyr	Cys
115								120					125		

Tyr	Asn	Ser	Ser	Asp	Thr	Trp	Thr	Asn	Ser	Cys	Ile	Pro	Glu	Ile	Ile
130								135					140		

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
 145 150 155 160
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
 165 170 175
 Thr Ile Pro Ala Pro Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
 180 185 190
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
 195 200 205
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
 210 215 220
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Val Pro Thr Ala Leu
 225 230 235 240
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Gly Leu Gly Phe
 245 250 255
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
 260 265 270
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
 275 280 285
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
 290 295 300
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
 305 310 315 320
 Glu Val

<210> 202
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 202
 gagcttcca tccaggtgtc atgc

24

<210> 203
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
 <400> 203		
gtcagtgaca gtacctactc gg		22
 <210> 204		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
 <220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
 <400> 204		
tggagcagga ggagtagtag tagg		24
 <210> 205		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
 <220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
 <400> 205		
aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt		50
 <210> 206		
<211> 1620		
<212> DNA		
<213> Homo sapiens		
 <220>		
<221> modified_base		
<222> (973)		
<223> a, t, c or g		
 <220>		
<221> modified_base		
<222> (977)		
<223> a, t, c or g		
 <220>		
<221> modified_base		
<222> (996)		
<223> a, t, c or g		
 <220>		
<221> modified_base		

<222> (1003)

<223> a, t, c or q

<400> 206

agatggcggt cttggcacct ctaattgctc tagtgttattc ggtgcgcga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg ccctgtctc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacggctcgc caacccaacg cgaagacggt aacccgttg 180
actttgaetg gagagaagtg gagatctga ttttctca gtcattgtg atgatgaaga 240
accgcagatc catcaactgtg gagcaacata taggcaacat ttcatgttt agtaaagtgg 300
ccaacacaat tctttcttc cgcttgata ttgcatggg cctactttac atcacactct 360
gcatagtgtt cctgatgacg tgcaaaccctt ccctatataat gggccctgag tatatcaagt 420
acttcaatga taaaaccatt gatgaggaaac tagaacggga caagagggtc acttggattg 480
tggagttctt tgccaattgg tctaattgact gccaatcatt tgcccctatc tatgctgacc 540
tctcccttaa atacaactgt acagggtctaa attttggaa ggtggatgtt ggacgctata 600
ctgatgttag tacgcggtaa aaagtggaca catcaccctt caccaagcaa ctccctaccc 660
tgatccctgtt ccaagggtggc aaggaggca tgccggcggcc acagattgac, aagaaaggac 720
gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaatgagc 780
tataccagcg ggccaagaaaa ctatcaaagg ctggagacaa tatccctgag gaggcgcctg 840
tggcttcaac cccccaccaca gtgtcagatg ggaaaacaa gaaggataaa taagatccctc 900
actttggcag tgcttcctct cctgtcaatt ccaggctt tccataacca caagcctgag 960
gctcagcct ttnattnatg tttccctt ggctngact ggntgggca gcatgcagct 1020
tctgatttt aagaggcatc tagggatttgc tcaaggccaccc tacaggaagg cctgccatgc 1080
tgtggccaaac tgtttcaactg gagcaagaaaa gagatctcat aggacggagg gggaaatgtt 1140
ttccctccaa gcttgggtca gtgtgttaac tgcttatcat ctattcagac atctccatgg 1200
tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca cagttgggt 1260
agaccttagat ttaaccctaa ggtaagatgc tgggtatag aacgctaaga attttccccc 1320
aaggactctt gcttccttaa gcccttctgg ctcgtttat ggtcttcatt aaaagtataa 1380
gcctaacttt gtgcgttagt ctaaggagaa acctttaacc acaaagttt tatcattgaa 1440
gacaatattg aacaaccctt tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500
actttccctt gtgtggtagg acttggagga gaaatccctt ggacttcac taaccctctg 1560
acatactccc cacaccccaqt tqatqqctt ccctaataaa aaqattqqqa tttccctttq 1620

<210> 207

<211> 296

<212> PRT

<213> *Homo sapiens*

<400> 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg

7

5

10

15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
20 25 30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
35 40 45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
50 55 60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
65 70 75 80

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
 85 90 95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
 100 105 110

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
 115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys
 130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val
 145 150 155 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile
 165 170 175

Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
 180 185 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val
 195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln
 210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg
 225 230 235 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn
 245 250 255

Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp
 260 265 270

Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser
 275 280 285

Asp Gly Glu Asn Lys Lys Asp Lys
 290 295

<210> 208
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 208
 gcttggatat tcgcatgggc ctac

<210> 209
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 209
tggagacaat atccctgagg 20

<210> 210
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 210
aacagttggc cacagcatgg cagg 24

<210> 211
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 211
ccatttatgt ggaacttagaa cgggacaaga gggtaacttg gatttgtggag 50

<210> 212
<211> 1985
<212> DNA
<213> Homo sapiens

<400> 212
ggacagctcg cgccccccga gagctctagc cgtcgaggag ctgcctgggg acgtttgcc 60
tggggcccca gcctggcccg ggtcacccctg gcatgaggag atgggcctgt tgctccttgt 120
cccattgtctc ctgctgcccc gctcctacgg actgcccttc tacaacggct tctactactc 180
caacagcgcc aacgaccaga acctaggcaa cggtcatggc aaagacctcc ttaatggagt 240
gaagctggtg gtggagacac ccgaggagac cctgttcaacc taccaagggg ccagtgttat 300
cctgccctgc cgctaccgct acgagccggc cctggctctcc ccgcggcgtg tgcgtgtcaa 360
atggtgaaag ctgtcggaga acggggccccc agagaaggac gtgctggtgg ccatcgggct 420
gaggcaccgc tcctttgggg actaccaagg cccgcgtgcac ctgcggcagg acaaagagca 480
tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatggcggtt accgctgtga 540
ggtcattgac gggctggagg atgaaagcg 600

ctttccttac cagtccccc acgggcgcta ccagttcaac ttccacgagg gccagcagg 660
 ctgtgcagag caggctgccc tggtggcctc cttttagcag ctcttccggg cctgggagga 720
 gggcctggac tggtcaacg cgggctggct gcaggatgct acggtgcaatg accccatcat 780
 gttcccccg cagccctgcg gtggccagg cctggcacct ggcgtgcgaa gctacggccc 840
 cgccaccgc cgccctgcacc gctatgatgt attctgcttc gctactgccc tcaagggcg 900
 ggtgtactac ctggagcacc ctgagaagct gacgctgaca gaggcaagg aggccctgcca 960
 ggaagatgat gccacgatcg ccaagggtgg acagctctt gccgcctgga agttccatgg 1020
 cctggaccgc tgacgctg gctggctggc agatggcagg gtccgcctacc ctgtgggttca 1080
 cccgcattcct aactgtggc ccccagagcc tggggtccga agcttggct tccccgaccc 1140
 gcagagccgc ttgtacggtg tttactgcta ccgcgcagcac taggacctgg gcccctcccc 1200
 tgccgcattc cctcactggc tgtgtattta ttgagtggtt cgtttccct tgggggttgg 1260
 agccattta actgtttta tacttctcaa tttaaatttt cttaaacat tttttacta 1320
 tttttgtaa agcaaacaga acccaatgcc tcccttgc cctggatgccc ccactccagg 1380
 aatcatgctt gctccctgg gccatttgcg gttttgtggg cttctggagg gttcccccggc 1440
 atccaggctg gtcctccctcc cttaggagg ttgggtccca gagtggcgg tggctgtct 1500
 agaatgccgc cgggagtccg ggcattgggg gcacagttt ccctccccct cagcctgggg 1560
 gaagaagagg gcctcggggg cctccggagc tgggctttgg gcctctactg cccacctcta 1620
 cttctctgtg aagccgctga ccccagtcg cccactgagg ggctagggct ggaagccagt 1680
 tctaggcttc caggcgaaat ctgagggaaag gaagaaactc ccctccccgt tccctttccc 1740
 ctctcggttc caaagaatct gttttgttgc catttgttcc tcctgtttcc ctgtgtgggg 1800
 aggggcctc agtgtgtgt actttggaca ataaatggtg ctatgactgc cttccgccaa 1860
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
 aaaaaa 1985

<210> 213
 <211> 360
 <212> PRT
 <213> Homo sapiens

<400> 213
 Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Pro Gly Ser Tyr
 1 5 10 15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
 20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
 35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
 50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
 65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
 85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
 100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

115	120	125	
Val Ser Leu Glu Ile Gln Asp	Leu Arg Leu Glu Asp	Tyr Gly Arg Tyr	
130	135	140	
Arg Cys Glu Val Ile Asp Gly	Leu Glu Asp Glu Ser Gly	Leu Val Glu	
145	150	155	160
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr	Gln Ser Pro Asn Gly Arg		
165	170	175	
Tyr Gln Phe Asn Phe His Glu Gly	Gln Gln Val Cys Ala Glu Gln Ala		
180	185	190	
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly			
195	200	205	
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr			
210	215	220	
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly	Pro Gly Leu Ala Pro		
225	230	235	240
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp			
245	250	255	
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu			
260	265	270	
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu			
275	280	285	
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys			
290	295	300	
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser			
305	310	315	320
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu			
325	330	335	
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr			
340	345	350	
Gly Val Tyr Cys Tyr Arg Gln His			
355	360		
<210> 214			
<211> 18			
<212> DNA			
<213> Artificial Sequence			
<220>			

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 215

ttccacctgtg gggtggag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 216

agggctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 217

agccagttag gaaatgcg

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 218

tgtccaaagt acacacacacct gagg

24

```

<210> 219
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 219
gatgccacga tcgccaaggt gggacagctc tttgcccgcct ggaag 45

<210> 220
<211> 1503
<212> DNA
<213> Homo sapiens

<400> 220
ggagagcgga gcgaagctgg ataacagggg accgatgatg tggcgaccat cagttctgct 60
gcttctgttg ctactgaggc acggggccca ggggaagcca tccccagacg caggccctca 120
tggccagggg agggtgcacc aggcggccccc cctgagcgcac gctcccatg atgacgccc 180
cggyaacttc cagtagcacc atgaggctt cttgggacgg gaagtggcca aggaattcga 240
ccaactcacc ccagaggaaa gccaggcccg tctggggcgg atcgtggacc gcatggaccc 300
cgcggggac ggcgacggct gggtgtcgct ggccgagctt cgcgctgga tcgcccacac 360
gcagcagcgg cacatacggg actcggtag cgcggcctgg gacacgtacg acacggaccc 420
cgacgggcgt gtgggttggg aggagctcg caacgcccacc tatggccact acgcgcccc 480
tgaagaattt catgacgtgg aggtgcaga gacctacaaa aagatgtgg ctggggacga 540
gcggcggttc cgggtggccg accaggatgg ggactcgatg gccactcgag aggagctgac 600
agccttcctg caccggcagg agttccctca catgcgggac atcgtgattt ctgaaacct 660
ggaggacctg gacagaaaaca aagatggcta tgtccaggtt gaggagtaca tcgcccatt 720
gtactcagcc gagcctgggg aggaggagcc ggctgggtt cagacggaga ggcagcagg 780
ccgggacttc cggatctga acaaggatgg gacactggat gggagtggg tggggccactg 840
ggtgctgccc cctggccagg accagccctt ggtggaaagcc aaccacctgc tgcacgagag 900
cgacacggac aaggatgggc ggctgagcaa agcggaaatc ctggtaatt ggaacatgtt 960
tgtggcagt caggccacca actatggcgaa ggacctgacc cggcaccacg atgagctgt 1020
agcacccgccc acctggccaca gcctcagagg cccgcacaat gaccggagga gggccgcgt 1080
tggctggcc ccctccctgt ccaggccccg caggaggcag atgcagtccc aggcatcc 1140
ctggccctgg gctctcaggg accccctggg tcggcttctg tccctgtcac acccccaacc 1200
ccagggaggg gctgtcatag tcccagagga taagcaatac ctatttctga ctgagtctcc 1260
cagcccagac ccagggaccc ttggcccca gctcagctt aagaaccgccc ccaaccctc 1320
cagtcacaaa tctgagcctc caccacatag actgaaactc ccctggcccc agccctctcc 1380
tgcctggcct ggcctggac acctcctctc tgccaggagg caataaaaagc cagcgccggg 1440
accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaa 1503

<210> 221
<211> 328
<212> PRT
<213> Homo sapiens

<400> 221
Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Arg His

```

1	5	10	15
Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly			
20	25	30	
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala			
35	40	45	
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val			
50	55	60	
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu			
65	70	75	80
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp			
85	90	95	
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg			
100	105	110	
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp			
115	120	125	
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly			
130	135	140	
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr			
145	150	155	160
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp			
165	170	175	
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu			
180	185	190	
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr			
195	200	205	
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu			
210	215	220	
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Pro Ala			
225	230	235	240
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn			
245	250	255	
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro			
260	265	270	
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu			
275	280	285	

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 225
 cccccctgag cgacgctccc ccatgatgac gcccacggga actt 44
 <210> 226
 <211> 2403
 <212> DNA
 <213> Homo sapiens
 <400> 226
 ggggccttgc ctccgcact cgggcgcagc cgggtggatc tcgaggcaggc gcggagcccc 60
 gggcgccggg cgcgggtgcg agggatccct gacgcctctg tccctgtttc tttgtcgctc 120
 ccagcctgtc tgcgtcggtt ttggcgcccc cgcctcccg cggtgccggg ttgcacaccc 180
 atccctggct tcgctcgatt tgccgcgcag ggcgcctccca gacctagagg ggcgcgtggcc 240
 tggagcagcg ggtcgctgtgt gtcctcttc ctctgcgcgc cggccggga tccgaagggt 300
 gcggggctct gaggaggtga cgcgcggggc ctccgcacc ctggccttgc cgcattctc 360
 cctctctccc aggtgtgagc agcctatcag tcaccatgtc cgcagcctgg atcccgctc 420
 tcggcctcgg tgcgtgtctg ctgctgctgc cggggcccg cggcagcgc gtagccgctc 480
 ccattgctat cacatgtttt accagaggct tgacatcag gaaagagaaa gcaagatgtcc 540
 tctgccagg gggctgcccctt gggctgaaat totctgtgtt tgggaacata gtatatgctt 600
 ctgtatcgag catatgtggg gctgctgtcc acaggggagt aatcagcaac tcagggggac 660
 ctgtacgat ctatagccta cctggctcgag aaaactattc ctcaatcgat gccaatggca 720
 tccagtcata aatgctttct agatggctgt ctctttcac agtaactaaa gcaaaaaga 780
 gtacacagga gcccacagga caagcagtgt ccacagcaca tccaccaaca gtaaacacgac 840
 taaagaaaaac acccgagaag aaaactggca ataaagattt taaagcagac attgcatttc 900
 tgattgtatgg aagctttat attgggcagc gccgatttaa ttacagaag aattttgtt 960
 gaaaagtggc tctaattgtt ggaattggaa cagaaggacc acatgtggc cttgttcaag 1020
 ccagtgaaca tccaaaata gaattttact tggaaaaactt tacatcagcc aaagatgtt 1080
 tggttgcctt aaaggaagta gggttcagag gggtaatttcaatacagga aagccttga 1140
 agcatactgc tcagaaattt ttcacggtag atgctggagt aagaaaaggg atccccaaag 1200
 tgggtgggtt atttattgtt ggttggcctt ctgtatgacat cgaggaagca ggcattgtgg 1260
 ccagagagtt tggtgtcaat gtatttatac tttctgtggc caagctatc cctgaagaa 1320
 tggggatggt tcaggatgtc acattttgtt acaaggctgt ctgtcggaaat aatggcttc 1380
 tctcttacca catgcccac tggtttggca ccacaaaata cgtaaagcct ctggtacaga 1440
 agctgtgcac tcatgaacaa atgatgtca gcaagacctt ttataactca gtgaacattt 1500
 cctttctaat tggatggctcc agcagtgtt gggatggcaat tttccgcctc atgcttgaat 1560
 ttgtttccaa catagccaaatg acttttggaa tctcggacat tgggtggcaag atagctgtc 1620
 tacagtttac ttatgtatcg cgcacggagt tcagtttccat gactatagc accaaagaga 1680
 atgtccatgc tgcgtatcaga aacatccgtt atatgatgtt tggaaacagct actgggtatg 1740
 ccatttcctt cactgtttaga aatgtgtttt gcccataaag ggagagcccc aacaagaact 1800
 tccttagtaat tgcacagat gggcagtctt atgatgtatgtt ccaaggccctt gcaatcgctc 1860
 cacatgtatgc agaaatcact atcttctctg ttgggtgtggc tggggcacctt ctggatgacc 1920
 tggaaagatat ggcttctaaa ccgaaggagt ctacgcctt ctgcataaaga gatgtcacag 1980
 gattagaacc aattgtttctt gatgtatca gaggcattttt tagagatttcc ttggaaatccc 2040
 agcaataatg gtaacatttt gacaactgaa agaaaaagta caaggggatc cagttgttac 2100
 attgtattct cataataactg aaatgttta gcaatctaga atcagatataa aaactattaa 2160
 gtatgtcaac agccatattttag gcaaaataagc actccctttaa agccgtgtcc ttctggttac 2220
 aatttacagt gtactttgtt aaaaacactg ctgaggcttc ataatcatgg ctcttagaaa 2280
 ctcagggaaag aggagataat gtggattttt accttaagag ttcttaaccat gcctactaaa 2340
 tgcacatcata tggaaattcc atagctcaat aaaagaatct gataacttaga ccaaaaaaaaa 2400
 aaa 2403

<210> 227

<211> 550
<212> PRT
<213> Homo sapiens

<400> 227
Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu
1 5 10 15

Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile
20 25 30

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
35 40 45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
50 55 60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
65 70 75 80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
85 90 95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
100 105 110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
115 120 125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
130 135 140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
145 150 155 160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
165 170 175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
180 185 190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
195 200 205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
210 215 220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
225 230 235 240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
245 250 255

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val
 260 265 270

Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val
 275 280 285

Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro
 290 295 300

Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys
 305 310 315 320

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp
 325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr
 340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
 355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg
 370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser
 385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
 405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
 420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp
 435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
 450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
 465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala His Asp Ala Gly Ile Thr Ile
 485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
 500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
 515 520 525

Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp
 530 535 540

Phe Leu Glu Ser Gln Gln
545 550

<210> 228
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 228
tggtctcgca caccgatc

18

<210> 229
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 229
ctgctgtcca caggggag

18

<210> 230
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 230
ccttgaagca tactgctc

18

<210> 231
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 231
gagatagcaa ttccgc

18

<210> 232

<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 232
ttcctcaaga gggcagcc 18

<210> 233
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 233
cttggcacca atgtccgaga ttcc 24

<210> 234
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 234
gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg 45

<210> 235
<211> 2586
<212> DNA
<213> Homo sapiens

<400> 235
cgccgcgcgc cccgacccgc ggcccgcgc cccgcgcgt cccgcacatctg cacccgcagc 60
ccggcgccct cccggcgaaa gcgagcagat ccagtccggc cccgcacgcga actcggtcca 120
gtcggggcgg cggctgcggg cgcaagcggc agatgcacgcg gcttggggcc accctgttgt 180
gcctgtgtct ggccggcgcc gtcacccacgg ccccgcgccc cgctccgcacg gcgacactgg 240
ctccagtcaa gcccggcccg gctctcagct acccgcagga ggaggccacc ctcaatgaga 300
tgttccgcga gtttggggaa ctgatggagg acacgcacgc caaatggcgc agcgcgggtgg 360
aagagatgaa ggcagaagaa gctgcgtcta aagcatcatc agaagtgaac ctggcaaact 420
tacctcccg ctatcacaat gagaccaaca cagacacgaa gtttggaaat aataccatcc 480
atgtgcaccc agaaattcac aagataacca acaaccagac tggacaaatg gtctttcag 540
agacagttt cacatctgtt ggagacgaaag aaggcagaag gagccacgag tgcatcatcg 600
acgaggactg tggggccacg atgtactgcc agtttgccag cttccagtac acctgccagc 660
catgccgggg coagaggatg ctctgcaccc gggacagtga gtgctgttga gaccagctgt 720

gtgtctgggg tcactgcacc aaaatggcca ccaggggcag caatggacc atctgtgaca 780
 accagaggga ctgccagccg gggctgtct gtgcattcca gagaggcctg ctgttccctg 840
 tgtgcacacc cctgcccgtg gaggggcagc tttgccatga ccccgccagc cggcttcgtg 900
 acctcatcac ctgggagcta gaggcctgtg gaggccttggc cggatgcct tggccactg 960
 gcctcctctg ccagccccac agccacagcc tgggttatgt gtgcaagccg accttcgtgg 1020
 ggagccgtga ccaagatggg gagatcctgc tgcccagaga ggtcccgat gagtatgaag 1080
 ttggcagctt catggaggag gtgcggcagg agctggagga cctggagagg agcctgactg 1140
 aagagatggc gctgggggg cctgcccgtg cccggcgtgc actgctggg ggggaagaga 1200
 ttttagatctg gaccaggctg tgggttagatg tgcaatagaa atagctaatt tatttcccc 1260
 ggtgtgtgct ttaggcgtgg gctgaccagg cttcttccta catcttcctt ccagtaagt 1320
 tccccctctgg cttgacagca tgaggtgtt tgcathtt cagctcccc aggctgttct 1380
 ccaggcttca cagtctggc tttggggag tcaggcaggg taaaactgca ggagcagttt 1440
 gccaccctg tccagattat tggctgctt gcctctacca gttggcagac agccgttgt 1500
 tctacatggc tttgataatt gtttgagggg aggagatgg aacaatgtgg agtctccctc 1560
 tgattgttt tggggaaatg tggagaagag tgccctgtt tgcaaacatc aacctggcaa 1620
 aaatgcaaca aatgaatttt ccacgcagtt cttccatgg gcataagttaa gctgtgcctt 1680
 cagctgtgc agatgaaatg ttctgttac cctgcattac atgtgtttat tcatccagca 1740
 gtgttgctca gtccttacct ctgtggcagg gcagcatttt catatccaag atcaattccc 1800
 tctctcagca cagcctgggg aggggggtcat tggcttcctc gtccatcagg gatctcagag 1860
 gctcagagac tgcagactgc ttggccaagt cacacagcta gtgaagacca gaggcagttc 1920
 atctgggtgt gactctaagc tcagtgtct ctccactacc ccacaccagc cttggtgcca 1980
 cccaaagtgc tccccaaaag gaaggagaat gggatttttc ttgaggcatg cacatctgga 2040
 attaaggcata aactaattct cacatccctc taaaagtaaa ctactgttag gaacagcagt 2100
 gttctcacag tggggcag ccgtccttctt aatgaagaca atgatattga cactgtccct 2160
 ctttggcagt tgcatttagta actttgaaag gtatatgact gagcgtagca tacagttaa 2220
 cctgcagaaa cagtagttttag gtaattgttag ggcgaggatt ataaatgaaa ttgcaaaaat 2280
 cacttagcag caactgaaga caattatcaa ccacgtggag aaaatcaaac cgagcagggc 2340
 tgtgtgaaac atgggtgtaa tatgcactg cgaacactga actctacgccc actccacaaa 2400
 tggatgtttc aggtgtcatg gactgttgcc accatgtatt catccagagt tcttaaagg 2460
 taaagttgca catgattgtta taagcatgt ttctttgagt tttaaattat gtataaaacat 2520
 aagttgcatt tagaaatcaa gcataaatca cttcaactgc aaaaaaaaaa aaaaaaaaaa 2580
 aaaaaaa 2586

<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

Met	Gln	Arg	Leu	Gly	Ala	Thr	Leu	Leu	Cys	Leu	Leu	Leu	Ala	Ala	Ala
1															15

Val	Pro	Thr	Ala	Pro	Ala	Pro	Ala	Pro	Thr	Ala	Thr	Ser	Ala	Pro	Val
															20
															25
															30

Lys	Pro	Gly	Pro	Ala	Leu	Ser	Tyr	Pro	Gln	Glu	Glu	Ala	Thr	Leu	Asn
															35
															40
															45

Glu	Met	Phe	Arg	Glu	Val	Glu	Glu	Leu	Met	Glu	Asp	Thr	Gln	His	Lys
															50
															55
															60

Leu	Arg	Ser	Ala	Val	Glu	Glu	Met	Glu	Ala	Glu	Glu	Ala	Ala	Ala	Lys
															65
															70
															75
															80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
 85 90 95

 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
 100 105 110

 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
 115 120 125

 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
 130 135 140

 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
 145 150 155 160

 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
 165 170 175

 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
 180 185 190

 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
 195 200 205

 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
 210 215 220

 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
 225 230 235 240

 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
 245 250 255

 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
 260 265 270

 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
 275 280 285

 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
 290 295 300

 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
 305 310 315 320

 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
 325 330 335

 Pro Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile
 340 345 350

<211> 17		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic oligonucleotide probe		
<400> 237		
ggagctgcac cccttgc		17
<210> 238		
<211> 49		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic Oligonucleotide Probe		
<400> 238		
ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg		49
<210> 239		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic Oligonucleotide Probe		
<400> 239		
gcagagcgga gatgcagcgg ct tg		24
<210> 240		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic Oligonucleotide Probe		
<400> 240		
ttggcagctt catggagg		18
<210> 241		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic Oligonucleotide Probe		
<400> 241		
cctgggcaaa aatgcaac		18

<210> 242
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 242
 ctccagctcc tggcgcacct cctc 24

<210> 243
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 243
 ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg 45

<210> 244
 <211> 3679
 <212> DNA
 <213> Homo Sapien

<400> 244
 aaggaggctg ggagggaaaga ggttaagaaag gtttagagaac ctacctcaca 50
 tctctctggg ctcagaagga ctctgaagat aacaataatt tcagccccatc 100
 cactctcctt ccctcccaa cacacatgtg catgtacaca cacacataca 150
 cacacataca ctttcctctc cttaactgaa gactcacagt cactcactct 200
 gtgagcaggt catagaaaag gacactaaag ctttaaggac aggccctggcc 250
 attacctctg cagtccttt ggcttgttga gtcaaaaaac atgggggggg 300
 ccaggcacgg tgactcacac ctgtaatccc agcattttgg gagaccgagg 350
 tgagcagatc acttgaggtc aggagttcga gaccagccctg gccaacatgg 400
 agaaaaccccc atctctacta aaaatacaaa aatttagccag gagtttgtgc 450
 aggtgcctgt aatcccagct actcaggtgg ctgagccagg agaatcgctt 500
 gaatccagga ggcggaggat gcagtcagct gagtgcacccg ctgcactcca 550
 gcctgggtga cagaatgaga ctctgtctca aacaaacaaa cacgggagga 600

gggttagata ctgcttctct gcaacccctc taactctgca tcctcttatt 650
ccagggctgc ccctgatggg gcctggcaat gactgagcag gcccagcccc 700
agaggacaag gaagagaagg catattgagg agggcaagaa gtgacgcccc 750
gtgtagaatg actgccctgg gagggtggtt cttggggccc tggcagggtt 800
gctgaccctt accctgaaa acacaaagag caggactcca gacttcctt 850
gtgaatggtc ccctgccctg cagctccacc atgaggcttc tcgtggcccc 900
actcttgcta gcttgggtgg ctggtgccac tgccactgtg cccgtggcac 950
cctggcatgt tcctgcccc cctcagtgtg cctgcccagat cccggccctgg 1000
tatacgcccc gtcgtccta ccgcgaggct accactgtgg actgcaatga 1050
cctattcctg acggcagtcc ccccggaact ccccgccaggc acacagaccc 1100
tgctcctgca gagcaacagc attgtccgtg tggaccagag tgagctggc 1150
tacctggcca attcacaga gctggacctg tcccagaaca gctttcgga 1200
tgcccgagac tgtgatttcc atgcctgca ccagctgctg agcctgcacc 1250
tagaggagaa ccagctgacc cggctggagg accacagctt tgcaaggctg 1300
gccagcctac aggaactcta tctcaaccac aaccagctt accgcatcgc 1350
ccccagggcc tttctggcc tcagcaactt gctgcggctg cacctcaact 1400
ccaacccctt gaggccatt gacagccgct ggttgaaat gctgccaac 1450
ttggagatac tcatgattgg cggcaacaag gtagatgcca tcctggacat 1500
gaacttccgg cccctggcca acctgcgtag cctggtgcta gcaggcatga 1550
acctgcggga gatctccgac tatgcctgg aggggctgca aagcctggag 1600
agccttcct tctatgacaa ccagctggcc cgggtggcca ggcgggcaact 1650
ggaacaggtg cccgggctca agttcctaga cctcaacaag aaccggctcc 1700
agcgggtagg gccgggggac tttgccaaca tgctgcacct taaggagctg 1750
ggactgaaca acatggagga gctggctcc atcgacaagt ttgccttgt 1800
gaacccccc gagctgacca agctggacat caccaataac ccacggctgt 1850
ccttcattca ccccccggcc ttccaccacc tgccccagat ggagaccctc 1900
atgctcaaca acaacgctt cagtgcttgc caccagcaga cgggtggagtc 1950

cctgcccaac ctgcaggagg taggtctcca cggcaacccc atccgctgtg 2000
 actgtgtcat ccgctgggcc aatgccacgg gcaccctgtt ccgattcatac 2050
 gagccgaat ccaccctgtg tgccggagcct ccggacctcc agccgcctccc 2100
 ggtccgtgag gtgccttcc gggagatgac ggaccactgt ttgccttc 2150
 tctccccacg aagttcccc ccaaggctcc aggttagccag tggagagagc 2200
 atggtgctgc attgcgggc actggccgaa cccgaacccg agatctactg 2250
 ggtcactcca gctgggcttc gactgacacc tgcccatgca ggcaggaggt 2300
 accgggtgta ccccgagggg accctggagc tgccggaggt gacagcagaa 2350
 gaggcagggc tatacacctg tgtggccag aacctggtgg gggctgacac 2400
 taagacggtt agtgtggttg tggggcgtgc tctcctccag ccaggcaggg 2450
 acgaaggaca ggggctggag ctccgggtgc aggagaccca cccctatcac 2500
 atcctgctat ctggggtcac cccacccaaac acagtgtcca ccaacctcac 2550
 ctggtccagt gcctcctccc tccggggcca gggggccaca gctctggccc 2600
 gcctgcctcg gggaaacccac agctacaaca ttaccggct ccttcaggcc 2650
 acggagtaact gggcctgcct gcaagtggcc tttgctgatg cccacaccca 2700
 gttggcttgt gtatgggcca ggaccaaaga ggccacttct tgccacagag 2750
 ccttagggga tcgtcctggg ctcattgcca tcctggctct cgctgtcctt 2800
 ctccctggcag ctgggcttagc ggccacaccc ggcacaggcc aaccaggaa 2850
 gggtgtgggt gggaggcggc ctctccctcc agcctggct ttctgggct 2900
 ggagtgcggcc ttctgtccgg gttgtgtctg ctccctcggt cctgcctgg 2950
 aatccagggaa ggaagctgcc cagatcctca gaaggggaga cactgttgcc 3000
 accattgtct caaaaattctt gaagctcagc ctgttctcag cagtagagaa 3050
 atcacttagga ctactttta ccaaaagaga agcagtctgg gccagatgcc 3100
 ctgccaggaa agggacatgg acccacgtgc ttgaggcctg gcagctggc 3150
 caagacagat ggggctttgt ggcctgggg gtgcttctgc agccttgaaa 3200
 aagttgcctt tacctccttag ggtcacctct gctgccattc tgaggaacat 3250

ctccaaggaa caggagggac tttggctaga gcctcctgcc tccccatctt 3300
 ctctctgccc agaggctcct gggcctggct tggctgtccc ctacctgtgt 3350
 ccccggtctg caccccttcc tcttctcttt ctctgtacag tctcagttgc 3400
 ttgcttttgt gcctcctggg caagggctga aggaggccac tccatctcac 3450
 ctggggggc tgccctcaat gtgggagtga ccccaagccag atctgaagga 3500
 catttggag agggatgccc aggaacgcct catctcagca gcctgggctc 3550
 ggcattccga agctgacttt ctataggcaa ttttgtacct ttgtggagaa 3600
 atgtgtcacc tcccccaacc cgattcactc ttttctcctg ttttgtaaaa 3650
 aataaaaata aataataaca ataaaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

Met	Arg	Leu	Leu	Val	Ala	Pro	Leu	Leu	Leu	Ala	Trp	Val	Ala	Gly
1														15
Ala	Thr	Ala	Thr	Val	Pro	Val	Val	Pro	Trp	His	Val	Pro	Cys	Pro
														30
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser
														45
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu
														60
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu
														75
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly
														90
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe
														105
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu
														120
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His
														135
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His
														150
140														145

Asn Gln Leu Tyr Arg Ile Ala Pro Arg Ala Phe Ser Gly Leu Ser
 155 160 165
 Asn Leu Leu Arg Leu His Leu Asn Ser Asn Leu Leu Arg Ala Ile
 170 175 180
 Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met
 185 190 195
 Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg
 200 205 210
 Pro Leu Ala Asn Leu Arg Ser Leu Val Leu Ala Gly Met Asn Leu
 215 220 225
 Arg Glu Ile Ser Asp Tyr Ala Leu Glu Gly Leu Gln Ser Leu Glu
 230 235 240
 Ser Leu Ser Phe Tyr Asp Asn Gln Leu Ala Arg Val Pro Arg Arg
 245 250 255
 Ala Leu Glu Gln Val Pro Gly Leu Lys Phe Leu Asp Leu Asn Lys
 260 265 270
 Asn Pro Leu Gln Arg Val Gly Pro Gly Asp Phe Ala Asn Met Leu
 275 280 285
 His Leu Lys Glu Leu Gly Leu Asn Asn Met Glu Glu Leu Val Ser
 290 295 300
 Ile Asp Lys Phe Ala Leu Val Asn Leu Pro Glu Leu Thr Lys Leu
 305 310 315
 Asp Ile Thr Asn Asn Pro Arg Leu Ser Phe Ile His Pro Arg Ala
 320 325 330
 Phe His His Leu Pro Gln Met Glu Thr Leu Met Leu Asn Asn Asn
 335 340 345
 Ala Leu Ser Ala Leu His Gln Gln Thr Val Glu Ser Leu Pro Asn
 350 355 360
 Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys
 365 370 375
 Val Ile Arg Trp Ala Asn Ala Thr Gly Thr Arg Val Arg Phe Ile
 380 385 390
 Glu Pro Gln Ser Thr Leu Cys Ala Glu Pro Pro Asp Leu Gln Arg
 395 400 405
 Leu Pro Val Arg Glu Val Pro Phe Arg Glu Met Thr Asp His Cys

410	415	420
Leu Pro Leu Ile Ser Pro Arg Ser Phe Pro Pro Ser Leu Gln Val		
425	430	435
Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu		
440	445	450
Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu		
455	460	465
Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly		
470	475	480
Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr		
485	490	495
Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val		
500	505	510
Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu		
515	520	525
Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His		
530	535	540
Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn		
545	550	555
Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr		
560	565	570
Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr		
575	580	585
Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala		
590	595	600
Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr		
605	610	615
Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly		
620	625	630
Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly		
635	640	645
Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly		
650	655	660
Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser		
665	670	675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp
680 685 690
Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu
695 700 705
Leu Pro Pro Leu Ser Gln Asn Ser
710

<210> 246
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 246
aacaaggtaa gatgccatcc tg 22

<210> 247
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 247
aaacttgtcg atggagacca gctc 24

<210> 248
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 248
aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249
<211> 3401
<212> DNA
<213> Homo Sapien

<400> 249
gcaaggccaag ggcgtgtttg agaaggtgaa gaagttccgg acccatgtgg 50
aggagggggaa cattgtgtac cgcctctaca tgcggcagac catcatcaag 100
gtgatcaagt tcatcctcat catctgctac accgtctact acgtgcacaa 150

catcaaggttc gacgtggact gcaccgtgga cattgagagc ctgacggct 200
accgcaccta ccgctgtgcc cacccctgg ccacactctt caagatcctg 250
gcgtccctct acatcagcct agtcatctt tacggcctca tctgcatgta 300
cacactgtgg tggatgctac ggcgctccct caagaagtac tcgtttgagt 350
cgatccgtga ggagagcagc tacagcgaca tccccgacgt caagaacgac 400
ttcgccttca tgctgcacct cattgaccaa tacgaccgc tctactccaa 450
gcgcgttcgccc gtcttcctgt cgagggttag tgagaacaag ctgcggcagc 500
tgaacctcaa caacgagtgg acgctggaca agctccggca gcggctcacc 550
aagaacgcgc aggacaagct ggagctgcac ctgttcatgc tcagtggcat 600
ccctgacact gtgttgacc tggtgagct ggaggtcctc aagctggagc 650
tgcgtccctg cgtgaccatc ccgcccagca ttgcccagct cacgggcctc 700
aaggagctgt ggctctacca cacagcggcc aagattgaag cgcctgcgt 750
ggccttcctg cgcgagaacc tgcggcgct gcacatcaag ttcaccgaca 800
tcaaggagat cccgctgtgg atctatagcc tgaagacact ggaggagctg 850
cacctgacgg gcaacctgag cgcgagaac aaccgctaca tcgtcatcga 900
cgggctgcgg gagctcaaac gcctcaaggt gctgcggctc aagagcaacc 950
taagcaagct gccacaggtg gtcacagatg tggcggtgca cctgcagaag 1000
ctgtccatca acaatgaggg caccaagctc atcgtcctca acagcctcaa 1050
gaagatggcg aacctgactg agctggagct gatccgctgc gacctggagc 1100
gcattccccca ctccatcttc agcctccaca acctgcagga gattgacctc 1150
aaggacaaca acctcaagac catcgaggag atcatcagct tccagcacct 1200
gcaccgcctc acctgcctta agctgtggta caaccacatc gcctacatcc 1250
ccatccagat cgccaacctc accaacctgg agcgcctcta cctgaaccgc 1300
aacaagatcg agaagatccc cacccagctc ttctactgcc gcaagctgcg 1350
ctacctggac ctcagccaca acaacctgac cttcctccct gccgacatcg 1400
gcctcctqca qaacctccaaq aacctaqcca tcacqqccaa ccggatcgag 1450

acgctccctc cgagacttt ccagtgcgg aagctgcggg ccctgcacct 1500
 gggcaacaac gtgctgcagt cactgcctc cagggtgggc gagctgacca 1550
 acctgacgca gatcgagctg cggggcaacc ggctggagtg cctgcctgtg 1600
 gagctggcg agtgcggact gctcaagcgc agcggcttg tggtggagga 1650
 ggacctgttc aacacactgc cacccgaggt gaaggagcgg ctgtggaggg 1700
 ctgacaagga gcaggcctga gcgaggccgg cccagcacag caagcagcag 1750
 gaccgctgcc cagtcctcag gcccgagggg gcaggcctag cttctcccag 1800
 aactcccgga cagccaggac agcctgcgg ctggcagga gcctggggcc 1850
 gtttgtgagt cagggcagag cgagaggaca gtatctgtgg ggctggcccc 1900
 ttttctccct ctgagactca cgtccccag ggcaagtgt ttttgtggag 1950
 agcaagtctc aagagcgcag tatttggata atcagggtat cttccctgga 2000
 ggccagctct gccccagggg ctgagctgcc accagaggc ctgggaccct 2050
 cacttagtt ctggtagttt attttctcc atctcccaacc tccttcatcc 2100
 agataactta tacattccca agaaagttca gcccagatgg aaggtgttca 2150
 gggaaaggtg ggctgccttt tccccctgtc cttatttagc gatgccgccc 2200
 ggcatttaac acccacctgg acttcagcag agtggccgg ggcgaaccag 2250
 ccatgggacg gtcacccagc agtgcggggc tgggctctgc ggtgcgggtcc 2300
 acgggagagc aggactccag ctggaaaggc caggcctgga gcttgcctct 2350
 tcagtttttggcagttt agttttttgt ttttttttt ttatcaaaa 2400
 aaacaatttt tttaaaaaaa aagctttgaa aatggatggt ttgggtatta 2450
 aaaagaaaaaa aaaaacttaa aaaaaaaaaaag acactaacgg ccagttagtt 2500
 ggagtctcag ggcagggtgg cagttccct tgagcaaagc agccagacgt 2550
 tgaactgtgt ttcccttccc tgggcgcagg gtgcagggtg tcttccggat 2600
 ctgggtgtac ctgggtccag gagttctatt tggcctggg gagggaggtt 2650
 tttttgttttggcagttt ttttttttttgc tcttgccttcc ttttcctcc 2700
 atgtgtcttgcagggcactc atttctgtgg ctgtcggcca gagggaatgt 2750
 tctggagctg ccaaggaggg aggagactcg ggttggctaa tcccccggatg 2800

aacggtgctc cattcgacc tccccctcgtgcctgccc tgccctctcca 2850
 cgcacagtgt taaggagcca agaggagcca cttcgcccag actttgttc 2900
 cccacacctt gggcatggg tgtgtccagt gccaccgctg gcctccgctg 2950
 cttccatca gccatcgcc acctggctt tcataaagag cagacactta 3000
 gaggctggc gggaaatgggg aggtcgcccc tgggaggggca ggcgttggtt 3050
 ccaagccgtt tcccgtccct ggccctgga gtgcacacag cccagtcggc 3100
 acctggtggc tggaaagccaa cctgcttttag atcaactcggtt tccccacatt 3150
 agaagggtcc ccgccttaga tcaatcacgt ggacactaag gcacgtttta 3200
 gagtcttttg tcttaatgtat tatgtccatc cgtctgtccg tccatttttg 3250
 ttttctgcgt cgtgtcattt gatataatcc tcagaaataa tgcacactag 3300
 cctctgacaa ccatgaagca aaaatccgtt acatgtgggt ctgaacttgt 3350
 agactcggtc acagtatcaa ataaaatcta taacagaaaa aaaaaaaaaa 3400
 a 3401

<210> 250

<211> 546
<212> PRT
<213> Homo Sapien

<400> 250

Met	Arg	Gln	Thr	Ile	Ile	Lys	Val	Ile	Lys	Phe	Ile	Leu	Ile	Ile
1														15

Cys Tyr Thr Val Tyr Tyr Val His Asn Ile Lys Phe Asp Val Asp

20														30
----	--	--	--	--	--	--	--	--	--	--	--	--	--	----

Cys Thr Val Asp Ile Glu Ser Leu Thr Gly Tyr Arg Thr Tyr Arg

35														45
----	--	--	--	--	--	--	--	--	--	--	--	--	--	----

Cys Ala His Pro Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe

50														60
----	--	--	--	--	--	--	--	--	--	--	--	--	--	----

Tyr Ile Ser Leu Val Ile Phe Tyr Gly Leu Ile Cys Met Tyr Thr

65														75
----	--	--	--	--	--	--	--	--	--	--	--	--	--	----

Leu Trp Trp Met Leu Arg Arg Ser Leu Lys Lys Tyr Ser Phe Glu

80														90
----	--	--	--	--	--	--	--	--	--	--	--	--	--	----

Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

95	100	105
Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro		
110	115	120
Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu		
125	130	135
Asn Lys Leu Arg Gln Leu Asn Leu Asn Glu Trp Thr Leu Asp		
140	145	150
Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu		
155	160	165
Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp		
170	175	180
Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val		
185	190	195
Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu		
200	205	210
Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala		
215	220	225
Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp		
230	235	240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu		
245	250	255
Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr		
260	265	270
Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu		
275	280	285
Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp		
290	295	300
Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr		
305	310	315
Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr		
320	325	330
Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser		
335	340	345
Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn		
350	355	360

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His
 365 370 375

 Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile
 380 385 390

 Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu
 395 400 405

 Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys
 410 415 420

 Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe
 425 430 435

 Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala
 440 445 450

 Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln
 455 460 465

 Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln
 470 475 480

 Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile
 485 490 495

 Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly
 500 505 510

 Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp
 515 520 525

 Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg
 530 535 540

 Ala Asp Lys Glu Gln Ala
 545

<210> 251
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 251
 caacaatgag ggcaccaagc 20

<210> 252
 <211> 24

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 252
 gatggctagg ttctggaggt tctg 24

 <210> 253
 <211> 47
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 253
 caacctgcag gagattgacc tcaaggacaa caacctaag accatcg 47

 <210> 254
 <211> 1650
 <212> DNA
 <213> Homo Sapien

 <400> 254
 gcctgttgct gatgctgccg tgccgtactt gtcatggagc tggcactgct 50

 gcgcctctccc gtcccgccgt ggttgtgtct gctgccgctg ctgtctggcc 100

 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150

 tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200

 ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcatgt 250

 ggcttcaggg cgggccagggc ggtagtgcata ctggatttgg aaacctttag 300

 gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350

 ccaggctgcc agtctcctat ttgtggataa tccccgtgggc actgggttca 400

 gttatgtgaa tggtagtggt gcctatgccc aggacctggc tatggtggt 450

 tcagacatga tggttctcct gaagacccctc ttcagttgcc acaaagaatt 500

 ccagacagtt ccattctaca ttttctcaga gtcctatgga ggaaaaatgg 550

 cagctggcat tggtctagag ctttataagg ccattcagcg agggaccatc 600

 aagtgcact ttgcgggggt tgccttgggt gattcctgga tctccccgt 650

 tgattcggtg ctctcctggg gaccttacct gtacagcatg tctttctcg 700

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn
 50 55 60

 Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln
 65 70 75

 Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu
 80 85 90

 Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp
 95 100 105

 Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr
 110 115 120

 Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu
 125 130 135

 Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe
 140 145 150

 Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser
 155 160 165

 Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu
 170 175 180

 Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly
 185 190 195

 Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu
 200 205 210

 Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys
 215 220 225

 Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala
 230 235 240

 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys
 245 250 255

 Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr
 260 265 270

 Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser
 275 280 285

 Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His
 290 295 300

 Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp		
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe		
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly		
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp		
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu		
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp		
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn		
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser		
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln		
440	445	450
 Gln Glu		
<210> 256		
<211> 1100		
<212> DNA		
<213> Homo Sapien		
 <400> 256		
ggccgcggga gaggaggcca tggcgcgcg cggggcgctg ctgctggcgc 50		
tgctgctggc tcgggctgga ctcaggaagc cggagtcgca ggaggcggcg 100		
ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatagtggg 150		
tggagaggac gccgaactcg ggctttggcc gtggcagggg agcctgcgcc 200		
tgtggattc ccacgtatgc ggagttagcc tgctcagcca ccgctggca 250		
ctcacggcgg cgcaactgctt tgaaacctat agtgacccta gtgatccctc 300		
cgggtggatg gtccagtttgc cagctgac ttccatgcca tccttctgga 350		
gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400		

cctcgctacc tgggaattc accctatgac attgccttgg tgaagctgtc 450
 tgcacctgtc acctacacta aacacatcca gccccatctgt ctccaggcct 500
 ccacatttga gtttgagaac cggacagact gctgggtgac tggctgggg 550
 tacatcaaag aggatgagggc actgccatct ccccacaccc tccaggaagt 600
 tcaggtcgcc atcataaaca actctatgtg caaccaccc ttcctcaagt 650
 acagtttccg caaggacatc tttggagaca tggtttgtgc tggcaacgcc 700
 caaggcggga aggatgcctg cttcggtgac tcaggtggac ccttggcctg 750
 taacaagaat ggactgtggt atcagattgg agtcgtgagc tggggagtgg 800
 gctgtggtcg gcccaatcgg ccgggtgtct acaccaatat cagccaccac 850
 tttgagtgga tccagaagct gatggcccag agtggcatgt cccagccaga 900
 cccctcctgg ccactactt tttccctct tctctggct ctcccaactcc 950
 tggggccggc ctgagcctac ctgagccat gcagcctggg gccactgcca 1000
 agtcaggccc tggttctctt ctgtcttggt tggtataaaa cacattccag 1050
 ttgatgcctt gcagggcatt cttcaaaaaa aaaaaaaaaa aaaaaaaaaa 1100

<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met	Gly	Ala	Arg	Gly	Ala	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Ala	Arg
1					5				10				15	

Ala	Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20		25		30										
----	--	----	--	----	--	--	--	--	--	--	--	--	--	--

Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly
						35		40			45		

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
						50		55		60				

Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
					65			70				75		

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
						80		85		90				

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser
 95 100 105

 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
 110 115 120

 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
 125 130 135

 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
 140 145 150

 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
 155 160 165

 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
 170 175 180

 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
 185 190 195

 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
 200 205 210

 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
 215 220 225

 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
 230 235 240

 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
 245 250 255

 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
 260 265 270

 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
 275 280 285

 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu
 290 295 300

 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
 305 310

 <210> 258
 <211> 2427
 <212> DNA
 <213> Homo Sapien

 <400> 258
 cccacgcgtc cgccggacgcg tggaaaggac agaatggac tccaaggctg 50

ctccttaggg ctctttgccccc tcatcccttc tggcaaatgc agttacagcc 100
 cggagcccgaa ccagcggagg acgctgcccc caggctgggt gtcctgggc 150
 cgtgcggacc ctgaggaaga gctgagtctc acctttgccccc tgagacagca 200
 gaatgtggaa agactctcgag cgtggtgca ggctgtgtcg gatcccagct 250
 ctcctcaata cggaaaatac ctgaccctag agaatgtggc tgatctggtg 300
 aggccatccc cactgaccct ccacacggtg caaaaatggc tcttggcagc 350
 cggagcccgag aagtgcatt ctgtgatcac acaggacttt ctgacttgct 400
 ggctgagcat ccgacaaggca gagctgctgc tccctggggc tgagtttcat 450
 cactatgtgg gaggacctac ggaaaccat gttgtaaggt ccccacatcc 500
 ctaccagctt ccacaggcct tggcccccca tgtggacttt gtggggggac 550
 tgcaccgttt tcccccaaca tcatccctga ggcaacgtcc tgagccgcag 600
 gtgacaggga ctgttaggcct gcatactgggg gtaacccctt ctgtgatccg 650
 taagcgatac aacttgacct cacaagacgt gggctctggc accagcaata 700
 acagccaagc ctgtgcccag ttccctggagc agtatttcca tgactcagac 750
 ctggctcagt tcatacgccct cttcggtggc aactttgcac atcaggcatc 800
 agtagcccgat gtggttggac aacagggccg gggccggggcc gggattgagg 850
 ccagtctaga tgtgcagtagc ctgatgagtg ctggtgccaa catctccacc 900
 tgggtctaca gtagccctgg ccggcatgag ggacaggagc cttccctgca 950
 gtggctcatg ctgctcagta atgagtcagc cctgccacat gtgcatactg 1000
 tgagctatgg agatgatgag gactccctca gcagcgccta catccagcgg 1050
 gtcaacactg agctcatgaa ggctgccgct cggggctca ccctgcttt 1100
 cgcctcaggt gacagtgggg cccgggtttg gtctgtctct ggaagacacc 1150
 agttccggccc tacctccct gcctccagcc cctatgtcac cacagtggga 1200
 ggcacatcct tccaggaacc tttccctcatc acaaatgaaa ttgtgacta 1250
 tatcagtgggt ggtggctca gcaatgtgtt cccacggct tcataccagg 1300
 aggaagctgt aacgaagttc ctgagctcta gcccccacct gccaccatcc 1350
 agttacttca atgccagtgcc cggtgcctac ccagatgtgg ctgcactttc 1400

tcatggctac tgggtggtca gcaacagagt gcccattcca tgggtgtccg 1450
 gaacctcgcc ctctactcca gtgtttgggg ggatcctatac cttgatcaat 1500
 gagcacagga tccttagtgg ccgcggccct cttggcttcc tcaacccaag 1550
 gctctaccag cagcatgggg caggtcttt tgatgttaacc cgtggctgcc 1600
 atgagtcctg tctggatgaa gaggttagagg gccagggtt ctgctctgg 1650
 cctggctggg atcctgttaac aggctggga acaccaactt cccagcttg 1700
 ctgaagactc tactcaaccc ctgacccttt cctatcagga gagatggctt 1750
 gtccccctgcc ctgaagctgg cagttcagtc ccttattctg ccctgttg 1800
 agccctgctg aaccctcaac tattgactgc tgcagacagc ttatctccct 1850
 aaccctgaaa tgctgtgagc ttgacttgac tcccaaccct accatgctcc 1900
 atcatactca ggtctcccta ctcctgcctt agattcctca ataagatgct 1950
 gtaactagca tttttgaat gcctctccct ccgcattctca tctttctt 2000
 ttcaatcagg cttttccaaa gggttgtata cagactctgt gcactatttc 2050
 acttgatatt cattccccaa ttcactgcaa ggagacctct actgtcaccg 2100
 ttactcttt cctaccctga catccagaaa caatggcctc cagtgcatac 2150
 ttctcaatct ttgctttatg gcctttccat catagttgcc cactccctct 2200
 ccttacttag cttccaggc ttaacttctc tgactactct tgtcttcctc 2250
 tctcatcaat ttctgcttct tcatggaatg ctgacccctca ttgtccatt 2300
 ttagattt tgctcttctc agtttactca ttgtccctg gaacaaatca 2350
 ctgacatcta caaccattac catctacta aataagactt tctatccaat 2400
 aatgattgat acctcaaatg taaaaaa 2427

<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met	Gly	Leu	Gln	Ala	Cys	Leu	Leu	Gly	Leu	Phe	Ala	Leu	Ile	Leu
1														
														15

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

20	25	30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu		
35	40	45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg		
50	55	60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln		
65	70	75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg		
80	85	90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala		
95	100	105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu		
110	115	120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly		
125	130	135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val		
140	145	150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro		
155	160	165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser		
170	175	180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly		
185	190	195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn		
200	205	210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln		
215	220	225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu		
230	235	240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala		
245	250	255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly		
260	265	270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala		
275	280	285

Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly
 290 295 300
 Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser
 305 310 315
 Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp
 320 325 330
 Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met
 335 340 345
 Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp
 350 355 360
 Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg
 365 370 375
 Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly
 380 385 390
 Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp
 395 400 405
 Tyr Ile Ser Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser
 410 415 420
 Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His
 425 430 435
 Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro
 440 445 450
 Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg
 455 460 465
 Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val
 470 475 480
 Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser
 485 490 495
 Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln
 500 505 510
 His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser
 515 520 525
 Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro
 530 535 540
 Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu
 545 550 555

Cys

<210> 260

<211> 1638

<212> DNA

<213> Homo Sapien

<400> 260

gccgcgcgct ctctccggc gcccacacct gtctgagcgg cgca gcgagc 50

cgcgccccgg gcgggctgct cggcgccgaa cagtgc tggc catggcagg 100

atccaggc tcctcttct tcttttctt ctgtctgtg ctgttggca 150

agttagccat tacagtgc cctggaaacc cacttggcct gcataaccgc 200

tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250

ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300

taagggact ccactgccc cttacgaaga ggccaagcaa tatctgtctt 350

atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcattc 400

tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450

ttcagggaaag tctcgaagga agcggcagat ttatggctat gacagcagg 500

tcagcatttt tgggaaggac ttcctgctca actaccctt ctcaacatca 550

gtgaagttat ccacgggctg cacccggcacc ctgggtggcag agaagcatgt 600

cctcacagct gcccactgca tacacgatgg aaaaacctat gtgaaaggaa 650

cccagaagct tcgagtgccc ttccctaaagc ccaagttaa agatggtggt 700

cgaggggcca acgactccac ttcagccatg cccgagcaga taaaatttca 750

gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaaggc 800

atgccaatga catcgccatg gattatgatt atgcccctcctt ggaactcaaa 850

aagccccaca agagaaaatt tatgaagatt ggggtgagcc ttcctgctaa 900

gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950

caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000

ttgctctacc agcaatgcga tgcccagcca ggggccagcg ggtctgggt 1050

ctatgtgagg atgtggaaga gacagcagca gaagtggag cgaaaaatta 1100

ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttcccccacag 1150
 gatttcaacg tggctgtcag aatcactcct ctcaaataatg cccagatttg 1200
 ctattggatt aaaggaaact acctggattg tagggagggg tgacacagtg 1250
 ttccctcctg gcagcaatta agggtcttca tgttcttatt ttaggagagg 1300
 ccaaattgtt ttttgtcatt ggctgcaca cgtgtgtgtg tgtgtgtgtg 1350
 tgtgtgttaag gtgtcttata atctttacc tatttcttac aattgcaaga 1400
 tgactggctt tactatttga aaactggttt gtgtatcata tcataatatca 1450
 tttaagcagt ttgaaggcat actttgcatt agaaataaaa aaaataactga 1500
 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgttttg 1550
 caaactttga ttttatttc atctgaactt gtttcaaaga tttatattaa 1600
 atattggca tacaagagat atgaaaaaaaaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Leu	Leu
1					5				10			15	

Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
					20				25			30		

Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr
					35				40			45		

Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu
					50				55			60		

Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
				65				70				75		

Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu
					80				85			90		

Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
					95				100			105		

Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
				110				115				120		

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser
 125 130 135

 Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe
 140 145 150

 Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val
 155 160 165

 Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly
 170 175 180

 Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu
 185 190 195

 Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr
 200 205 210

 Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys
 215 220 225

 Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
 230 235 240

 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro
 245 250 255

 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys
 260 265 270

 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp
 275 280 285

 Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu
 290 295 300

 Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala
 305 310 315

 Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln
 320 325 330

 Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp
 335 340 345

 Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg
 350 355 360

 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly
 365 370 375

 Asn Tyr Leu Asp Cys Arg Glu Gly
 380

<210> 262
<211> 1378
<212> DNA
<213> Homo Sapien

<400> 262
gcatcgccct gggctctcg agcctgctgc ctgctcccc gccccaccag 50
ccatgggtt ttctggagcg ccccccagccc tgggtgggg ctgtctcgcc 100
accttcacct ccctgctgct gctggcgtcg acagccatcc tcaatgcggc 150
caggataacct gttcccccag cctgtggaa gccccagcag ctgaaccggg 200
ttgtggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250
atccagaaga atgggaccca ccactgcgcgca ggttctctgc tcaccagccg 300
ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350
acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400
cggtcccaga aggtgggtgt tgccctgggtg gagccccacc ctgtgtattc 450
ctggaaggaa ggtgcctgtg cagacattgc cctggtgctg ctcgagcgct 500
ccatacagtt ctcagagcgg gtccctgcca tctgcctacc tgatgcctct 550
atccacactcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600
ccaagatgga gttcccttgc cccacccctca gaccctgcag aagctgaagg 650
ttccttatcat cgactcgaa gtctgcagcc atctgtactg gcggggagca 700
ggacaggaccc ccatcaactga ggacatgctg tgtgccggct acttggaggg 750
ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800
tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggtgt 850
gccgagcgca acaggccccgg ggtctacatc agcctctctg cgcacccgctc 900
ctgggtggag aagatcgtgc aagggttgca gctccgggg cgcgctcagg 950
gggttggggc cctcaggcga ccgagccagg gctctggggc cgccgcgcgc 1000
tccttagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050
cacatctgga tctggatctg cggcggcctc gggcggttcc ccccgccgta 1100
aataggctca tctacactcta cctctgggg cccggacggc tgctgcggaa 1150

aggaaaacccc ctcccccggacc cgccccgacgg cctcaggccc ccctccaagg 1200
 catcaggccc cgcccaacgg cctcatgtcc ccgcggccac gacttccggc 1250
 cccgcggcccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300
 ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350
 ataaattttt tattctccaa aaaaaaaaa 1378

 <210> 263
 <211> 317
 <212> PRT
 <213> Homo Sapien

 <400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu
1				5					10				15	
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu
				20					25				30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
				35					40				45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu
				50				55					60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
				65				70					75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His
				80					85				90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu
				95					100				105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys
				110					115				120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys
				125					130				135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser
				140					145				150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala
				155					160				165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp
				170					175				180	

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu
 185 195

Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His
 200 210

Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met
 215 225

Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
 230 240

Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu
 245 255

Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
 260 270

Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val
 275 285

Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly
 290 300

Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala
 305 310 315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaaggttg 19

<210> 266

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 266
agctctagac caatgccagc ttcc 24

<210> 267
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 267
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 268
gggaaattca ccctatgaca ttgcc 25

<210> 269
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 269
gaatgccctg caagcatcaa ctgg 24

<210> 270
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 270
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 271
gcggaagggc agaatgggac tccaaag 26

<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 272
cagccctgcc acatgtgc 18

<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 273
tactgggtgg tcagcaac 18

<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 274
ggcgaagagc agggtgagac cccg 24

<210> 275
<211> 45

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 275
gcccctcatcc tctctggcaa atgcagttac agccccggagc ccgac 45

<210> 276
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 276
gggcaggat tccagggttc c 21

<210> 277
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 277
ggctatgaca gcaggttc 18

<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 278
tgacaatgac cgaccagg 18

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 279
gcatcgatt gctggtagag caag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280
ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281
<211> 34
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281
cgtctcgagc gctccatata gttcccttgc cccca 34

<210> 282
<211> 61
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282
tggagggggga gcgggatgct tgtctggcg actccggggg cccccctcatg 50
tgccaggtgg a 61

<210> 283
<211> 119
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283
ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50
gcagccatct gtactggcg ggagcaggac agggaccat cactgaggac 100
atgctgtgtg ccggctact 119

<210> 284
<211> 1875
<212> DNA
<213> Homo Sapien

<400> 284
gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50
ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgttga tggtgagct gcacaacctc taccggggccc 150
 aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200
 ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250
 caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300
 gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350
 tacaacctca gcgccgcccac ctgcagccca ggccagatgt gcggccacta 400
 cacgcaggtg gtatgggcca agacagagag gatcggtgt ggttcccact 450
 tctgtgagaa gctccagggt gttgaggaga ccaacatcga attactggtg 500
 tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550
 ggggactccg tgctcccaat gtccctctgg ctaccactgc aagaactccc 600
 tctgtgaacc catcggaaagc ccggaagatg ctcaggatt gccttacctg 650
 gtaactgagg ccccatcctt ccggcgact gaagcatcag actctaggaa 700
 aatgggtact cttttccc tagcaacggg gattccggct ttcttggtaa 750
 cagaggtctc aggctccctg gcaaccaagg ctctgcgtgc tgtggaaacc 800
 caggccccaa cttccttagc aacgaaagac ccgcctcca tggcaacaga 850
 ggctccacct tgcgtAACAA ctgaggtccc ttccatTTG gcagtcaca 900
 gcctgcctc cttggatgag gagccagtta cttcccaaa atcgacccat 950
 gttccatcc caaaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000
 ctctaggagc ccagagaact ctctggaccc caagatgtcc ctgacagggg 1050
 caagggaaact cttcccat gcccaggagg aggctgaggt tgaggctgag 1100
 ttgcctcctt ccagtggagg ctggcctca gttttccag cccaggacaa 1150
 gccaggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200
 agtccctgcc caatttcccc aatacctctg ccaccgctaa tgccacgggt 1250
 gggcgtgcc tggctctgca gtcgtcctt ccagggtgcag agggccctga 1300
 caagccttagc gttgtgtcag ggctgaactc gggccctggt catgtgtggg 1350
 gcccctctcct gggactactg ctccctgcctc ctctgggttt ggctggaatc 1400

ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtcctcctgt 1450
 catcttcccc accctgtccc cagccctaa acaagatact tcttggttaa 1500
 ggccctccgg aaggaaagg ctacggggca tgtgcctcat cacaccatcc 1550
 atcctggagg cacaaggcct ggctggctgc gagtcagga ggccgcctga 1600
 ggactgcaca ccgggcccac acctctcctg cccctccctc ctgagtcctg 1650
 ggggtggag gatttggagg agctcaactgc ctacctggcc tggggctgtc 1700
 tgccccacaca gcatgtgcgc tctccctgag tgcctgtgtc gctggggatg 1750
 gggattccta gggcagatg aaggacaagc cccactggag tggggtttt 1800
 tgagtgggg aggcaaggac gagggaaagga aagtaactcc tgactctcca 1850
 ataaaaaacct gtccaaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu
1								10				15		

Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp
								20		25			30	

Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala
									35	40			45	

Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp
								50		55		60		

Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val
								65		70		75		

Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe
								80		85		90		

Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu
								95		100		105		

Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys
								110		115		120		

Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala
								125		130		135		

Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu
 140 145 150
 Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr
 155 160 165
 Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly
 170 175 180
 Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser
 185 190 195
 Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro
 200 205 210
 Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser
 215 220 225
 Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile
 230 235 240
 Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys
 245 250 255
 Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr
 260 265 270
 Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr
 275 280 285
 Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu
 290 295 300
 Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile
 305 310 315
 Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser
 320 325 330
 Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly
 335 340 345
 Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu
 350 355 360
 Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro
 365 370 375
 Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr
 380 385 390
 Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser
 395 400 405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
 410 415 420

 Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
 425 430 435

 Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
 440 445 450

 Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe
 455 460

<210> 286
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 286
 tcctgcagtt tcctgatgc 19

<210> 287
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 287
 ctcatattgc acaccagtaa ttcg 24

<210> 288
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 288
 atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289
 <211> 3662
 <212> DNA
 <213> Homo Sapien

<400> 289
 gtaactgaag tcaggctttt catttggaa gccccctcaa cagaattcgg 50

tcatttctcca agttatgggt gacgtacttc tgggtttctc cctctgcttg 100
ctttttcaca tttagcagacc ggacttaagt cacaacagat tatctttcat 150
caaggcaagt tccatgagcc accttcaaag cttcgagaa gtgaaactga 200
acaacaatga attggagacc attccaaatc tgggaccagt ctggcaaat 250
attacacttc tctccttggc tggaaacagg attgttgaaa tactccctga 300
acatctgaaa gagtttcagt ccctgaaac tttggacctt agcagcaaca 350
atatttcaga gctccaaact gcatttccag ccctacagct caaatatctg 400
tatctcaaca gcaaccgagt cacatcaatg gaacctgggt attttgacaa 450
tttggccaac acactccttg tgttaaagct gaacaggaac cgaatctcag 500
ctatcccacc caagatgtt aaactgcccc aactgcaaca tctgaatttgc 550
aaccgaaaca agattaaaaa tgttagatgga ctgacattcc aaggcattgg 600
tgctctgaag tctctgaaaa tgcaaagaaa tggagtaacg aaacttatgg 650
atggagctt ttgggggctg agcaacatgg aaattttgca gctggaccat 700
aacaacctaa cagagattac caaggctgg cttaacggct tgctgtatgct 750
gcaggaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800
cctggagtt ctgccagaag ctcagtgagc tggacctaacc ttcaatcac 850
ttatcaaggt tagatgattc aagcttcattt ggcctaagct tactaaatac 900
actgcacatt gggacaacaaca gagtcagcta cattgctgat tggcatttcc 950
gggggcttcc cagttaaag actttggatc tgaagaacaa tggaaatttcc 1000
tggactattt aagacatgaa tggtgcttcc tctgggcttg acaaactgag 1050
gcgactgata ctccaaggaa atcggatccg ttcttattact aaaaaaggcct 1100
tcactggttt ggatgcattt gaggcatctag acctgagtga caacgcaatc 1150
atgtctttac aaggcaatgc atttcacaa atgaagaaac tgcaacaatt 1200
gcatttaaat acatcaagcc ttttgtgcga ttgcccagctt aatggctcc 1250
cacagttgggt ggcggaaaac aactttcaga gctttgtaaa tgccagttgt 1300
gcccatcctc agctgctaaa aggaagaagc attttgctg ttagccccaga 1350

tggctttgtg tgtgatgatt ttcccaaacc ccagatcacg gttcagccag 1400
aaacacagtc ggcaataaaa gttccaatt tgagttcat ctgctcagct 1450
gccagcagca gtgattcccc aatgactttt gcttgaaaaa aagacaatga 1500
actactgcat gatgctgaaa tggaaaatta tgcacaccc tcggcccaag 1550
gtggcgaggt gatggaggt accaccatcc ttccggctgcg cgaggtggaa 1600
tttgcaggta agggaaata tcagtgtgtc atctccaatc actttggttc 1650
atcctactct gtcaaagcca agcttacagt aaatatgctt ccctcattca 1700
ccaagacccc catggatctc accatccgag ctggggccat ggcacgcttg 1750
gagtgctg ctgtggggca cccagcccc cagatagcct ggcagaagga 1800
tggggcaca gacttcccag ctgcacggga gagacgcattt catgtgatgc 1850
ccgaggatga cgtgttctt atcgtggatg tgaagataga ggacattggg 1900
gtatacagct gcacagctca gaacagtgcg ggaagtattt cagcaaatgc 1950
aactctgact gtcctagaaa caccatcatt tttgcggcca ctgtggacc 2000
gaactgtaac caagggagaa acagccgtcc tacagtgcattt tgctggagga 2050
agccctcccc ctaaaactgaa ctggacccaa gatgatagcc cattgggttgt 2100
aaccgagagg cactttttt cagcaggcaa tcagcttctg attattgtgg 2150
actcagatgt cagtgtatgc gggaaataca catgtgagat gtctaacacc 2200
cttggcactg agagagggaaa cgtgcgcctc agtgtgatcc ccactccaac 2250
ctgcgcactcc cctcagatga cagccccatc gtttagacgtt gacggatggg 2300
ccactgtggg tgcgtgatc atagccgtgg tttgctgtgt ggtggccacg 2350
tcactcgtgt ggggtggatcat catataccac acaaggcggaa ggaatgaaga 2400
ttgcagcatt accaacacag atgagaccaa cttgccagca gatattcccta 2450
gttatttgc atctcaggaa acgttagctg acaggcagga tgggtacgtg 2500
tcttcagaaaa gtggaaagcca ccaccagttt gtcacatctt caggtgctgg 2550
atttttctta ccacaacatg acagtagtgg gacctgccat attgacaata 2600
gcagtgaagc tgatgtggaa gctgccacag atctgttcct ttgtccgttt 2650
ttgggatcca caggccctat gtatttgaag ggaaatgtgt atggctcaga 2700

tcctttgaa acatatcata caggtgcag tcctgaccga agaacagttt 2750
 taatggacca ctatgagccc agttacataa agaaaaaggaa gtgctaccca 2800
 tgttctcatc cttcagaaga atcctgcga cggagctca gtaatatatc 2850
 gtggccttca catgtgagga agctacttaa cactagttac ttcacaatg 2900
 aaggacctgg aatgaaaaat ctgtgtctaa acaagtcctc tttagatttt 2950
 agtgcaaatc cagagccagc gtcgggtgcc tcgagtaatt ctcatggg 3000
 taccttgga aaagctctca ggagacctca cctagatgcc tattcaagct 3050
 ttggacagcc atcagattgt cagccaagag ctttttattt gaaagctcat 3100
 tcttccccag acttggactc tgggtcagag gaagatggga aagaaaggac 3150
 agatttcag gaagaaaatc acattgtac cttaaacag acttagaaaa 3200
 actacaggac tccaaatttt cagtcttatg acttggacac atagactgaa 3250
 tgagacccaa ggaaaagctt aacatactac ctcaagtcaa cttttattta 3300
 aaagagagag aatcttatgt ttttaaatg gagttatgaa tttaaaagg 3350
 ataaaaatgc ttattttata cagatgaacc aaaattacaa aaagttatga 3400
 aaattttat actggaaatg atgctcatat aagaataacct tttaaacta 3450
 ttttttaact ttgtttatg caaaaaagta tcttacgtaa attaatgata 3500
 taaatcatga ttattttatg tattttata atgccagatt tcttttatg 3550
 gaaaatgagt tactaaagca ttttaataa tacctgcctt gtaccatitt 3600
 tttaatagaa gttacttcat tatatttgc acattatatt taataaaatg 3650
 tgtcaatttg aa 3662

<210> 290
 <211> 1059
 <212> PRT
 <213> Homo Sapien

<400> 290
 Met Val Asp Val Leu Leu Leu Phe Ser Leu Cys Leu Leu Phe His
 1 5 10 15
 Ile Ser Arg Pro Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
 20 25 30

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
 35 40 45

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
 50 55 60

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
 65 70 75

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
 80 85 90

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
 95 100 105

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
 110 115 120

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
 125 130 135

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
 140 145 150

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn
 155 160 165

Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala
 170 175 180

Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met
 185 190 195

Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu
 200 205 210

Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly
 215 220 225

Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn
 230 235 240

Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu
 245 250 255

Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser
 260 265 270

Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn
 275 280 285

Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser

290	295	300
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile		
305	310	315
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
320	325	330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
335	340	345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
350	355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
365	370	375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp		
425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala		
440	445	450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser		
455	460	465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu		
470	475	480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln		
485	490	495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu		
500	505	510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn		
515	520	525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn		
530	535	540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg		
545	550	555

Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro
 560 565 570
 Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro
 575 580 585
 Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val
 590 595 600
 Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser
 605 610 615
 Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr
 620 625 630
 Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp
 635 640 645
 Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala
 650 655 660
 Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
 665 670 675
 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
 680 685 690
 Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
 695 700 705
 Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val
 710 715 720
 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
 725 730 735
 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
 740 745 750
 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
 755 760 765
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys
 770 775 780
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
 785 790 795
 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
 800 805 810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 815 820 825
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
 830 835 840
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
 845 850 855
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
 860 865 870
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
 875 880 885
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
 890 895 900
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
 905 910 915
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
 920 925 930
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
 935 940 945
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
 950 955 960
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
 965 970 975
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
 980 985 990
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
 995 1000 1005
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
 1010 1015 1020
 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
 1025 1030 1035
 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro
 1040 1045 1050
 Asn Phe Gln Ser Tyr Asp Leu Asp Thr
 1055
 <210> 291
 <211> 2906

<212> DNA

<213> Homo Sapien

<400> 291

ggggagagga attgaccatg taaaaggaga cttttttt tggtggtggt 50
ggctgttggg tgccttgcaa aaatgaagga tgcaggacgc agctttctcc 100
tggAACCGAA CGCAATGGAT AAACtGATTG TGCAAGAGAG AAGGAAGAAC 150
gaagctttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200
acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250
ttggtgtgtt ctgacataaa taaataatct taaagcagct gttcccctcc 300
ccaccccca aaaaaaggat gattggaaat gaagaaccga ggattcacaa 350
agaaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400
gatattttg gaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450
ggtgtggtgg tgtttcctt tcttttgaa tttcccacaa gaggagagga 500
aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550
gcagattgag gcattgattt gggagagaa accagcagag cacagttgga 600
tttgtgccta tgttgactaa aattgacgga taattgcagt tggattttc 650
ttcatcaacc tcctttttt taaatttttta ttcctttgg tatcaagatc 700
atgcgttttca tcttgttctt aaccacctgg atttccatct ggatgttgct 750
gtgatcagtc tgaaatacaa ctgttgaat tccagaagga ccaacaccag 800
ataaaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850
ataggtccta ggttaacag ggcctattt gacccctgc ttgtggtgct 900
gctggctctt caacttcttg tggggctgg tctggcgg gctcagacct 950
ggaaaaacc tgcgtgaggc tccggatggc atctccacca acacacggct 1000
gctgaacctc catgagaacc aaatccagat catcaaagt aacagcttca 1050
agcacttgag gcacttggaa atcctacagt tgagtaggaa ccatatcaga 1100
accattgaaa ttggggcttt caatggtctg gcgAACCTCA acactctgga 1150
actcttgac aatcgcttta ctaccatccc gaatggagct tttgtatact 1200
actcttgac aatcgcttta ctaccatccc gaatggagct tttgtatact 1250

tgtctaaact gaaggagctc tggttgcgaa acaacccat taaaagcatc 1300
ccttcttatg ctttaacag aattccttct ttgcgccgac tagacttagg 1350
ggaattgaaa agactttcat acatctcaga aggtgcctt gaaggtctgt 1400
ccaacttgag gtatttgaac cttgcccattgt gcaaccctcg ggaaatccct 1450
aacctcacac cgctcataaa actagatgag ctggatctt ctggaatca 1500
tttatctgcc atcaggcctg gctcttcca gggtttgatg caccttcaaa 1550
aactgtggat gatacagtcc cagattcaag tgattgaacg gaatgcctt 1600
gacaaccttc agtcactagt ggagatcaac ctggcacaca ataatctaac 1650
attactgcct catgacctct tcactccctt gcatcatcta gagcggatac 1700
atttacatca caacccttgg aactgtaact gtgacatact gtggctcagc 1750
tggtgataa aagacatggc cccctcgaac acagcttggt gtgcccggtg 1800
taacactcct cccaatctaa aggggaggta cattggagag ctgcaccaga 1850
attacttcac atgctatgct ccggtgattt tggagcccc tgcagacctc 1900
aatgtcactg aaggcatggc agctgagctg aaatgtcggg cctccacatc 1950
cctgacatct gtatcttggta ttactccaaa tggAACAGTC atgacacatg 2000
gggcgtacaa agtgccgata gctgtgctca gtgatggtaac gttaaatttc 2050
acaaatgtaa ctgtgcaaga tacaggcatg tacacatgta tggtagtaa 2100
ttccgttggg aatactactg cttcagccac cctgaatgtt actgcagcaa 2150
ccactactcc tttctcttac ttttcaaccg tcacagtaga gactatggaa 2200
ccgtctcagg atgaggcacg gaccacagat aacaatgtgg gtcccaactcc 2250
agtggtcgac tgggagacca ccaatgtgac cacctctctc acaccacaga 2300
gcacaaggta gacagagaaa acottcacca tcccagtgac tggatataaac 2350
agtggatcc caggaattga tgaggtcatg aagactacca aaatcatcat 2400
tgggtttt gtggccatca cactcatggc tgcagtgtatg ctggtcattt 2450
tctacaagat gaggaagcag caccatcgac aaaaccatca cgccccaaca 2500
aggactgttg aaattattaa tgtggatgtatg gagattacgg gagacacacc 2550

catggaaagc cacctgcccc tgcctgctat cgagcatgag cacctaaatc 2600
 actataactc atacaaatct cccttcaacc acacaacaac agttaacaca 2650
 ataaattcaa tacacagttc agtgcattgaa cccgttattga tccgaatgaa 2700
 ctctaaagac aatgtacaag agactcaa at ctaaaacatt tacagagtta 2750
 caaaaaacaa acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800
 tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaaacaa 2850
 aaaagaaaag aaatttattt attaaaaattt ctattgtat ctaaaggaga 2900
 caaaaa 2906

<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

Met	Leu	Asn	Lys	Met	Thr	Leu	His	Pro	Gln	Gln	Ile	Met	Ile	Gly
1														15
Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
														30
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
														45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
														60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
														75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
														90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
														105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
														120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
														135
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
														150
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

2000-2005-0000

155	160	165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly		
170	175	180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly		
185	190	195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg		
200	205	210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp		
215	220	225
?		
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln		
230	235	240
Gly Leu Met His Leu Lys Leu Trp Met Ile Gln Ser Gln Ile		
245	250	255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val		
260	265	270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp		
275	280	285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His		
290	295	300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp		
305	310	315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys		
320	325	330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp		
335	340	345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro		
350	355	360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys		
365	370	375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn		
380	385	390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val		
395	400	405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp		
410	415	420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr
425 430 435

Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro
440 445 450

Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser
455 460 465

Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro
470 475 480

Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro
485 490 495

Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr
500 505 510

Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr
515 520 525

Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala
530 535 540

Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His
545 550 555

Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn
560 565 570

Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu
575 580 585

Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser
590 595 600

Tyr Lys Ser Pro Phe Asn His Thr Thr Val Asn Thr Ile Asn
605 610 615

Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn
620 625 630

Ser Lys Asp Asn Val Gln Glu Thr Gln Ile
635 640

<210> 293
<211> 4053
<212> DNA

<213> Homo Sapien

<400> 293
agccgacgct gctcaagctg caactctgtt gcagttggca gttctttcg 50

gtttcctcc tgctgttgg gggcatgaaa gggcttcgcc gccgggagta 100
 aaagaaggaa ttgaccgggc agcgcgaggg aggagcgccc acgcgaccgc 150
 gagggcgggc gtgcaccttc ggctggaagt ttgtgccggg ccccgagcgc 200
 gcgcggctg ggagcttcgg gtagagacct aggccgctgg accgcgatga 250
 gcgcggccgag cctccgtcgc cgccgcggg gggtgggct gctgctgtgc 300
 gcggtgctgg ggccgcgtgg ccggtccgac agcggcggc gcgggaaact 350
 cgggcagccc tctgggttag ccgcgcagcg cccatgc(cc) actacctgcc 400
 gctgcctcgg ggacctgctg gactgcagtc gtaagcggct agcgcgtatt 450
 cccgagccac tcccgtcctg ggtcgctcgg ctggacttaa gtcacaacag 500
 attatcttc atcaaggcaa gttccatgag ccaccttcaa agccttcgag 550
 aagtgaaact gaacaacaat gaattggaga ccattccaaa tctggacca 600
 gtctcggcaa atattacact tctctccttgc gctggaaaca ggattgttga 650
 aataactccct gaacatctga aagagttca gtcccttgcg actttggacc 700
 ttagcagcaa caatatttca gagctccaaa ctgcatttcc agccctacag 750
 ctcaaataatc tgtatctcaa cagcaaccga gtcacatcaa tggaacctgg 800
 gtattttgac aatttggcca acacactcct tgtgttaaag ctgaacagga 850
 accgaatctc agctatccca cccaaagatgt ttaaactgcc ccaactgcaa 900
 catctcgaat tgaaccgaaa caagattaaa aatgttagatg gactgacatt 950
 ccaaggcctt ggtgctctga agtctctgaa aatgcaaaga aatggagtaa 1000
 cggaaacttat ggatggagct ttttggggc tgagcaacat ggaaattttg 1050
 cagctggacc ataacaacct aacagagatt accaaaggct ggctttacgg 1100
 cttgctgatg ctgcaggaac ttcatctcag cccaaatgcc atcaacagga 1150
 tcagccctga tgcctggag ttctgccaga agctcagtga gctggaccta 1200
 actttcaatc acttatcaag gtttagatgtat tcaagcttcc ttggcctaag 1250
 cttactaaat acactgcaca ttgggaacaa cagagtcagc tacattgctg 1300
 attgtgcctt cggggggctt tccagttaa agactttggta tctgaagaac 1350

aatgaaattt cctggactat tgaagacatg aatggtgctt tctctggct 1400
 tgacaaactg aggcgactga tactccaagg aaatcgatc cgttctatta 1450
 ctaaaaaagc cttcaactggt ttggatgcattt gggcatct agacctgagt 1500
 gacaacgcaa tcatagtcttt acaaggcaat gcattttcac aaatgaagaa 1550
 actgcaacaa ttgcatttaa atacatcaag cctttgtgc gattgccagc 1600
 taaaatggct cccacagtgg gtggcggaaa acaactttca gagctttgta 1650
 aatgccagtt gtgcccattcc tcagctgcta aaaggaagaa gcattttgc 1700
 tgttagccca gatggctttg tgtgtgatga ttttcccaaa cccagatca 1750
 cggttcagcc agaaacacag tcggcaataa aaggttccaa tttgagttc 1800
 atctgctcag ctgccagcag cagtgattcc ccaatgactt ttgcttggaa 1850
 aaaagacaat gaactactgc atgatgctga aatggaaaat tatgcacacc 1900
 tccggccca aggtggcgag gtgatggagt ataccaccat cttcggctg 1950
 cgcgaggtgg aatttgcag tgaggggaaa tatcagtgtc tcatactccaa 2000
 tcacttttgtt tcatactact ctgtcaaagc caagcttaca gtaaatatgc 2050
 ttccctcatt caccaagacc cccatggatc tcaccatccg agctggggcc 2100
 atggcacgct tggagtgtgc tgctgtgggg cacccagccc cccagatagc 2150
 ctggcagaag gatgggggca cagacttccc agctgcacgg gagagacgca 2200
 tgcatagtgat gcccgaggat gacgtgttct ttatcgtgga tgtgaagata 2250
 gaggacatttgggatacag ctgcacagct cagaacagtg caggaagtat 2300
 ttcagcaaat gcaactctga ctgtcctaga aacaccatca ttttgcggc 2350
 cactgttggta ccgaactgta accaaggag aaacagccgt cctacagtgc 2400
 attgctggag gaagccctcc ccctaaactg aactggacca aagatgatag 2450
 cccatgggtg gtaaccgaga ggcactttt tgcagcaggc aatcagcttc 2500
 tgattattgt ggactcagat gtcagtgtatg ctggaaata cacatgtgag 2550
 atgtctaaca cccttggcac tgagagagga aacgtgcgcc tcagtgat 2600
 ccccaactcca acctgcgact cccctcagat gacagccccca tcgttagacg 2650
 atgacggatg ggccactgtg ggtgtcgtga tcatacgccgt ggtttgctgt 2700

gtgggtggca cgtcactcgt gtgggtggtc atcatataacc acacaaggcg 2750
 gaggaatgaa gattgcagca ttacccaacac agatgagacc aacttgccag 2800
 cagatattcc tagttatttg tcatctcagg gaacgttagc tgacaggcag 2850
 gatgggtacg tgccttcaga aagtggaagc caccaccagt ttgtcacatc 2900
 ttcaggtgct ggatttttct taccacaaca tgacagtagt gggacctgcc 2950
 atattgacaa tagcagtgaa gctgatgtgg aagctgccac agatctgttc 3000
 ctgtccgt ttttggatc cacaggccct atgtatttga agggaaatgt 3050
 gtatggctca gatccttttgc aaacatatca tacaggttgc agtcctgacc 3100
 caagaacagt tttaatggac cactatgagc ccagttacat aaagaaaaag 3150
 gagtgctacc catgttctca tccttcagaa gaatcctgct aacggagctt 3200
 cagtaatata tcgtggcctt cacatgtgag gaagctactt aacactagtt 3250
 actctcacaa tgaaggaccc ggaatgaaaa atctgtgtct aaacaagtcc 3300
 tcttttagatt ttagtgcaaa tccagagcca gcgtcggttg cctcgagtaa 3350
 ttctttcatg ggtacccccc gaaaagctct caggagacct cacctagatg 3400
 cctattcaag ctttggacag ccatcagatt gtcagccaaag agccttttat 3450
 ttgaaagctc attcttcccc agacttggac tctgggttag aggaagatgg 3500
 gaaagaaaagg acagattttc aggaagaaaa tcacatttgt accttaaac 3550
 agactttaga aaactacagg actccaaatt ttcaagtctt tgacttggac 3600
 acatagactg aatgagacca aaggaaaaagc ttaacataact acctaagtg 3650
 aacttttatt taaaagagag agaatcttattt gttttttaaa tggagttatg 3700
 aattttaaaa ggataaaaaat gctttatata tacagatgaa ccaaaattac 3750
 aaaaagttat gaaaattttt atactggaa tgatgctcat ataagaatac 3800
 ctttttaaac tattttttaa ctttggatc tgcaaaaaag tatcttacgt 3850
 aaattaatga tataaatcat gatttttttata tgtatTTTtaatgccaga 3900
 tttttttta tggaaaatga gttactaaag cattttaaat aatacctgcc 3950
 ttgtaccatt tttaaatag aagttacttc attatattt gcacattata 4000

tttaataaaa tgtgtcaatt tgaaaaaaaaaaaaaaa 4050

aaa 4053

<210> 294

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

Met	Ser	Ala	Pro	Ser	Leu	Arg	Ala	Arg	Ala	Ala	Gly	Leu	Gly	Leu
1					5				10				15	

Leu	Leu	Cys	Ala	Val	Leu	Gly	Arg	Ala	Gly	Arg	Ser	Asp	Ser	Gly
					20				25				30	

Gly	Arg	Gly	Glu	Leu	Gly	Gln	Pro	Ser	Gly	Val	Ala	Ala	Glu	Arg
					35				40				45	

Pro	Cys	Pro	Thr	Thr	Cys	Arg	Cys	Leu	Gly	Asp	Leu	Leu	Asp	Cys
						50			55				60	

Ser	Arg	Lys	Arg	Leu	Ala	Arg	Leu	Pro	Glu	Pro	Leu	Pro	Ser	Trp
					65				70				75	

Val	Ala	Arg	Leu	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
					80				85				90	

Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu
					95				100				105	

Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser
					110				115				120	

Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu
					125				130				135	

Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu
					140				145				150	

Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro
					155				160				165	

Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr
					170				175				180	

Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu
					185				190				195	

Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys
					200				205				210	

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

215	220	225
Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala		
230	235	240
Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met		
245	250	255
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu		
260	265	270
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly		
275	280	285
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn		
290	295	300
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu		
305	310	315
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser		
320	325	330
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn		
335	340	345
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser		
350	355	360
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile		
365	370	375
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
380	385	390
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
395	400	405
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
410	415	420
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
425	430	435
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
440	445	450
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
455	460	465
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
470	475	480

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp
 485 490 495
 Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala
 500 505 510
 Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser
 515 520 525
 Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu
 530 535 540
 Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln
 545 550 555
 Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu
 560 565 570
 Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn
 575 580 585
 His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn
 590 595 600
 Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg
 605 610 615
 Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro
 620 625 630
 Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro
 635 640 645
 Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val
 650 655 660
 Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser
 665 670 675
 Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr
 680 685 690
 Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp
 695 700 705
 Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala
 710 715 720
 Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
 725 730 735
 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
 740 745 750

Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
 755 760 765
 Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val
 770 775 780
 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
 785 790 795
 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
 800 805 810
 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
 815 820 825
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Asn Glu Asp Cys
 830 835 840
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
 845 850 855
 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
 860 865 870
 Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 875 880 885
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
 890 895 900
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
 905 910 915
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
 920 925 930
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
 935 940 945
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
 950 955 960
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
 965 970 975
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
 980 985 990
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
 995 1000 1005
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu

	1010	1015	1020
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn			
1025	1030	1035	
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu			
1040	1045	1050	
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg			
1055	1060	1065	
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly			
1070	1075	1080	
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn			
1085	1090	1095	
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro			
1100	1105	1110	
Asn Phe Gln Ser Tyr Asp Leu Asp Thr			
1115			
<210> 295			
<211> 18			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Synthetic Oligonucleotide Probe			
<400> 295			
ggaaccgaat ctcagcta 18			
<210> 296			
<211> 19			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Synthetic Oligonucleotide Probe			
<400> 296			
cctaaactga actggacca 19			
<210> 297			
<211> 19			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Synthetic Oligonucleotide Probe			

<400> 297
ggctggagac actgaacct 19

<210> 298
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 298
acagctgcac agctcagaac agtg 24

<210> 299
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 299
cattcccaagt ataaaaattt tc 22

<210> 300
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 300
gggtcttgggt gaatgagg 18

<210> 301
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 301
gtgcctctcg gttaccacca atgg 24

<210> 302
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 302
gcggccactg ttggaccgaa ctgtAACCAA gggagAAACA gccgtcctac 50

<210> 303
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 303
gccttgaca acttcagtc actagtgg 28

<210> 304
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 304
ccccatgtgt ccatgactgt tccc 24

<210> 305
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 305
tactgcctca tgacctcttc actcccttgc atcatcttag agcgg 45

<210> 306
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 306
actccaAGGA aatcgGATCC gtTC 24

<210> 307
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 307
ttagcagctg aggatggca caac 24

<210> 308
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 308
actccaagga aatcgatcc gttc 24

<210> 309
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 309
gccttcactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310
<211> 3296
<212> DNA
<213> Homo Sapien

<400> 310

caaaaacttgc gtcgcggaga gcgcaggct tgacttgaat ggaaggagcc 50
cgagcccccg gagcgcagct gagactgggg gagcgcgttc ggcctgtggg 100
gcgcgcgtcg ggcgcggggc gcagcaggaa agggaaagct gtggctgtcc 150
ctgttccacg aggccacact ggtgtgaacc gggagagccc ctgggtggtc 200
ccgtcccccta tccctccctt atataaaaaac cttccacact ggaaaggcag 250
cgccgaggca ggagggctca tggtgagcaa ggaggccggc tgatctgcag 300
gcgcacagca ttccgagttt acagattttt acagatacca aatggaaggc 350
gaggaggcag aacagcctgc ctgggtccat cagccctggc gcccaggcgc 400

atctgactcg gcacccctg caggcaccat gcccccagagc cgggtgctgc 450
tgctcctgct gctgctgccg ccacagctgc acctgggacc tgtgcttgcc 500
gtgagggccc caggatttgg ccgaagtggc gcccacagcc tgagccccga 550
agagaacgaa tttgcggagg aggagccggt gctggtaactg agccctgagg 600
agcccccggcc tggcccagcc gcggtcagct gcccccgaga ctgtgcctgt 650
tcccaggagg gcgtcgtgga ctgtggcggt attgacctgc gtgagttccc 700
gggggacactg cctgagcaca ccaaccacact atctctgcag aacaaccagc 750
tggaaaagat ctacccttag gagctctccc ggctgcacccg gctggagaca 800
ctgaacacctgc aaaacaacccg cctgacttcc cgagggctcc cagagaaggc 850
gtttgagcat ctgaccaacc tcaattacct gtacttggcc aataacaagc 900
tgaccttggc accccgcttc ctgccaaacg ccctgatcag tgtggacttt 950
gctgccaact atctcaccaa gatctatggg ctcaccttg gccagaagcc 1000
aaacttgagg tctgtgtacc tgcacaacaa caagctggca gacgccgggc 1050
tgccggacaa catgttcaac ggctccagca acgtcgaggt cctcatcctg 1100
tccagcaact tcctgcgcca cgtgccccaa cacctgcccctg ccctgtta 1150
caagctgcac ctcaagaaca acaagctgga gaagatcccc ccggggccct 1200
tcagcgagct gagcagcctg cgcgagctat acctgcagaa caactacctg 1250
actgacgagg gcctggacaa cgagaccttc tggaaagctct ccagcctgga 1300
gtacctggat ctgtccagca acaacctgtc tcgggtccca gctggctgc 1350
cgcgccgcct ggtgctgctg cacttggaga agaacgcctt ccggagcggt 1400
gacgcgaatg tgctgacccc catccgcagc ctggagtacc tgctgctgca 1450
cagcaaccag ctgcgggagc agggcatcca cccactggcc ttccaggggcc 1500
tcaagcggtt gcacacgggt cacctgtaca acaacgcgtt ggagcgcggt 1550
cccagtggcc tgcctcgccg cgtgcgcacc ctcatgatcc tgcacaacca 1600
gatcacagggc attggcccgcg aagactttgc caccacctac ttccctggagg 1650
agctcaacct cagctacaac cgcatcacca gcccacaggt gcaccgcgac 1700

gccttcggca agctgcgcct gctgcgctcg ctggacctgt cggcaaccg 1750
gctgcacacg ctgccacctg ggctgcctcg aaatgtccat gtgctgaagg 1800
tcaagcgcaa ttagctggct gccttggcac gaggggcgtt ggccggcatg 1850
gctcagctgc gtgagctgta cctcaccaggc aaccgactgc gcagccgagc 1900
cctggggccc cgtgcctggg tggacctcgcc ccatctgcag ctgctggaca 1950
tcgcccggaa tcagctcaca gagatccccg aggggctccc cgagtcactt 2000
gagtacctgt acctgcagaa caacaagatt agtgcggtgtc ccgccaatgc 2050
cttcgactcc acgccccacc tcaaggggat ctttctcagg tttaacaagc 2100
tggctgtggg ctccgtggtg gacagtgcct tccggaggct gaagcacctg 2150
caggtcttgg acattgaagg caacttagag tttggtgaca tttccaagga 2200
ccgtggccgc ttggggaaagg aaaaggagga ggaggaagag gaggaggagg 2250
aggaagagga aacaagatag tgacaagggt atgcagatgt gacctaggat 2300
gatggaccgc cggaactcttt tctgcagcac acgcctgtgt gctgtgagcc 2350
ccccactctg ccgtgctcac acagacacac ccagctgcac acatgaggca 2400
tcccacatga cacgggctga cacagtctca tatccccacc cttcccaacg 2450
gcgtgtccca cggccagaca catgcacaca catcacaccc tcaaacaccc 2500
agctcagcca cacacaacta ccctccaaac caccacagtc tctgtcacac 2550
ccccactacc gctgccacgc cctctgaatc atgcagggaa gggtotgccc 2600
ctgcccggc acacacaggc acccattccc tccccctgtt gacatgtgt 2650
tgcgtatgca tacacaccac acacacacac atgcacaagt catgtgcgaa 2700
cagccctcca aagcctatgc cacagacagc tcttgccccca gccagaatca 2750
gccatagcag ctcgccgtct gccctgtcca tctgtccgtc cgttccctgg 2800
agaagacaca aggttatcca tgctctgtgg ccaggtgcgtt gccacccct 2850
ggaactcaca aaagctggct tttattcctt tcccatccta tggggacagg 2900
agccttcagg actgctggcc tggcctggcc caccctgctc ctccaggtgc 2950
tggcagtcacatgca ctctgctaag agtccctccc tgccacgccc tggcaggaca 3000
caggcacttt tccaatgggc aagccccagtg gaggcaggat gggagagccc 3050

cctgggtgct gctgggcct tggggcagga gtgaagcaga ggtgatgggg 3100
 ctgggctgag ccagggagga aggacccagc tgcacctagg agacacctt 3150
 gttcttcagg cctgtgggg aagttccggg tgccttatt ttttattctt 3200
 ttctaaggaa aaaaatgata aaaatctcaa agctgattt tcttggtata 3250
 gaaaaactaa tataaaagca ttatccatat ccctgcaaaa aaaaaaa 3296

<210> 311
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 311
gcattggcccg cgagactttg cc 22

<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 312
gcggccacgg tccttgaaa tg 22

<210> 313
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 313
tggaggagct caacctcagc tacaaccgca tcaccagccc acagg 45

<210> 314
<211> 3003
<212> DNA
<213> Homo Sapien

<400> 314
gggagggggc tccgggcgcc gcgcagcaga cctgctccgg ccgcgcgcct 50
cgccgcgtgtc ctccggagc ggcagcagta gccccggcgg cgagggctgg 100

gggttcctcg agactctcag aggggcgcct cccatcgccg cccaccaccc 150
caacctgttc ctgcgcgc actgcgtgc gccccaggac ccgctgccc 200
acatggattt tctcctggcg ctggtgctgg tatcctcgct ctacctgcag 250
gcggccgccc agttcgacgg gaggtggccc aggcaaatacg tgtcatcgat 300
tggcctatgt cggtatggtg ggaggattga ctgctgctgg ggctggctc 350
gccagtcttg gggacagtgt cagcctgtgt gccaaccacg atgcaaacat 400
ggtgaatgta tcgggccaaa caagtgcagg tgcattcctg gttatgctgg 450
aaaaacctgt aatcaagatc taaatgagtg tggcctgaag cccggccat 500
gtaagcacag gtgcattgaa acttacggca gctacaaggc ctactgtctc 550
aacggatata tgctcatgca ggtatggtcc tgctcaaggc ccctgacctg 600
ctccatggca aactgtcagt atggctgtga tggatgtaaa ggacaaatac 650
ggtgccaggc cccatcccgt ggcctgcacc tggctcctga tgggaggacc 700
tgtgttagatg ttgatgaaatg tgctacagga agagcctcct gcccattt 750
taggcaatgt gtcaacactt ttgggagcta catctgcagg tgcataaaag 800
gcttcgatct catgtatatt ggaggcaaat atcaatgtca tgacatagac 850
gaatgctcac ttggtcagta tcagtcgcgc agctttgctc gatgttataa 900
cgtacgtggg tcctacaagt gcaaatgtaa agaaggatac cagggtgatg 950
gactgacttg tgttatatc ccaaaagtta tgattgaacc ttccaggc 1000
attcatgtac caaaggaaa tggtaccatt ttaaagggtg acacaggaaa 1050
taataattgg attcctgatg ttggaaagtac ttggcggcct ccgaagacac 1100
catatattcc tcctatcatt accaacaggc ctacttctaa gccaacaaca 1150
agacctacac caaagccaaac accaattcct actccaccac caccaccacc 1200
cctgccaaca gagctcagaa cacctctacc acctacaacc ccagaaaggc 1250
caaccaccgg actgacaact atagcaccag ctgcgtac acctccagga 1300
gggattacag ttgacaacag ggtacagaca gaccctcaga aaccctcagg 1350
agatgtgttc agtgttctgg tacacagttt taattttgac catggacttt 1400

gtggatggat cagggagaaa gacaatgact tgcactggga accaatcagg 1450
gaccacagcag gtggacaata tctgacagtg tcggcagcca aagccccagg 1500
gggaaaagct gcacgcttgg tgctacctct cggccgcctc atgcattcag 1550
gggacctgtg cctgtcattc aggacacaagg tgacggggct gcactctggc 1600
acactccagg tttttgttag aaaaacacggt gcccacggag cagccctgtg 1650
gggaagaaat ggtggccatg gctggaggca aacacagatc accttgcgag 1700
gggctgacat caagagcgaa tcacaaagat gattaaaggg ttggaaaaaaa 1750
agatctatga tggaaaatta aaggaactgg gattattgag cctggagaag 1800
agaagactga ggggcaaacc attgatggtt ttcaagtata tgaagggttg 1850
gcacagagag ggtggcgacc agctgttctc catatgcact aagaatagaa 1900
caagagggaaa ctggcttaga ctagagtata agggagcatt tcttggcagg 1950
ggccattgtt agaatacttc ataaaaaaaaa aagtgtgaaa atctcagtat 2000
ctctctctct ttctaaaaaaaaa ttagataaaaa atttgtctat ttaagatgg 2050
taaagatgtt cttacccaag gaaaagtaac aaattataga atttccaaaa 2100
agatgttttg atcctactag tagtatgcag tgaaaatott tagaactaaa 2150
taatttggac aaggcttaat ttaggcattt ccctcttgac ctcctaattgg 2200
agagggattg aaaggggaag agccccacaa atgctgagct cactgaaata 2250
tctctccctt atggcaatcc tagcagtatt aaagaaaaaa ggaaactatt 2300
tattccaaat gagagtatga tggacagata ttttagtac tcagtaatgt 2350
cctagtgtgg cggtggttt caatgttct tcatggtaaa ggtataagcc 2400
tttcatttgt tcaatggatg atgtttcaga tttttttttt ttaagagat 2450
ccttcaagga acacagttca gagagattt catcggtgc attctctctg 2500
cttcgtgtgt gacaagttat cttggctgct gagaaagagt gccctgcccc 2550
acacccggcag accttcctt cacctcatca gttatgattca gtttctctta 2600
tcaattggac tctcccaggt tccacagaac agtaatattt tttgaacaat 2650
aggtacaata gaaggtcttc tgtcattaa cctggtaaag gcagggctgg 2700
agggggaaaaa taaatcatta agcctttgag taacggcaga atatatggct 2750

gtagatccat ttttaatgtt tcatttcctt tatggtcata taactgcaca 2800
 gctgaagatg aaaggggaaa ataaatgaaa attttacttt tcgatgccaa 2850
 tgatacattg cactaaactg atggaagaag ttatccaaag tactgtataa 2900
 catcttgaaa attatataat gtttctaaa ataaaaaatg ttagtggttt 2950
 tccaaatggc ctaataaaaa caattatgg taaataaaaa cactgttagt 3000
 aat 3003

<210> 315
 <211> 509
 <212> PRT
 <213> Homo Sapien

<400> 315
 Met Asp Phe Leu Leu Ala Leu Val Leu Val Ser Ser Leu Tyr Leu
 1 5 10 15

Gln Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro Arg Gln Ile Val	20	25	30
---	----	----	----

Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys	35	40	45
---	----	----	----

Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys	50	55	60
---	----	----	----

Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys	65	70	75
---	----	----	----

Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu	80	85	90
---	----	----	----

Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met	95	100	105
---	----	-----	-----

Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met	110	115	120
---	-----	-----	-----

Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met	125	130	135
---	-----	-----	-----

Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg	140	145	150
---	-----	-----	-----

Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg	155	160	165
---	-----	-----	-----

Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys
 170 175 180
 Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys
 185 190 195
 Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr
 200 205 210
 Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys
 215 220 225
 Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys
 230 235 240
 Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr
 245 250 255
 Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro
 260 265 270
 Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn
 275 280 285
 Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro
 290 295 300
 Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr
 305 310 315
 Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro
 320 325 330
 Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr
 335 340 345
 Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala
 350 355 360
 Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln
 365 370 375
 Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val
 380 385 390
 His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu
 395 400 405
 Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly
 410 415 420
 Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys

425 430 435
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly
440 445 450
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser
455 460 465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala
470 475 480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln
485 490 495
Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg
500 505

<210> 316
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 316
gatggttcct gctcaagtgc cctg 24

<210> 317
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 317
ttgcacttgtt aggacccacg tacg 24

<210> 318
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 318
ctgatggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

<210> 319
<211> 2110
<212> DNA

<213> Homo Sapien

<400> 319

cttctttgaa aaggattatc acctgatcat gttctctctg catttgcccc 50
tttagattgt gaaatgtggc tcaaggtctt cacaacttcc ctttcctttg 100
caacaggtgc ttgctcgaaa ctgaaggtga cagtgccatc acacactgtc 150
catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200
cactccagca tcagacatcc agatcatatg gctattttag agaccccaca 250
caatgccccaa atacttactg ggctctgtga ataagtctgt ggttcctgac 300
ttggaataacc aacacaagtt caccatgatg ccacccaaatg catctctgct 350
tatcaacccca ctgcagttcc ctgatgaagg caattacatc gtgaaggtca 400
acattcaggg aaatggaact ctatctgcca gtcagaagat acaagtcacg 450
gttcatgtatc ctgtcacaaa gccagtggtg cagattcatc ctccctctgg 500
ggctgtggag tatgtggggaa acatgaccct gacatgccat gtggaaagggg 550
gcactcggct agcttaccaa tggctaaaaa atgggagacc tgtccacacc 600
agctccaccc actccttttc tccccaaaac aatacccttc atattgtcc 650
agtaaccaag gaagacattt ggaattacag ctgcctggtg aggaaccctg 700
tcagtgaaat ggaaagtgtatcattatgc ccatcatata ttatggacct 750
tatggacttc aagtgaattt tgataaaaggctaaaagttag gggaaagtgtt 800
tactgttgac cttggagagg ccattctatt tgattgtct gctgattctc 850
atccccccaa cacctactcc tggatttagga ggactgacaa tactacatat 900
atcatthaagc atgggcctcg cttagaagtt gcatctgaga aagtagcccc 950
gaagacaatg gactatgtgt gctgtgctta caacaacata accggcaggc 1000
aagatgaaac tcatttcaca gttatcatca cttccgtagg actggagaag 1050
cttgcacaga aaggaaaatc attgtcaccc tttagcaagta taactggaat 1100
atcactatcc ttgatttatc ccatgtgtct tctcttccta tgaaaaaaat 1150
atcaacccta caaagttata aaacagaaac tagaaggcag gccagaaaca 1200
gaatacagga aagctcaaaccatttcaggc catgaagatg ctctggatga 1250

cttcggata tatgaatttg ttgcgttcc agatgttct ggtgttcca 1300
 ggattccaag caggctgtt ccagcctctg attgtgtatc gggcaagat 1350
 ttgcacagta cagtgtatga agttattcag cacatccctg cccagcagca 1400
 agaccatcca gagtgaactt tcatggcta aacagtacat tcgagtgaaa 1450
 ttctgaagaa acatTTtaag gaaaaacagt gaaaaagtat attaatctgg 1500
 aatcagtgaa gaaaccagga ccaacacctc ttactcatta ttccttaca 1550
 tgcagaatag aggcatTTT gcaaattgaa ctgcaggTT ttcagcatat 1600
 acacaatgtc ttgtgcaaca gaaaaacatg ttggggaaat attcctcagt 1650
 ggagagtcgt tctcatgctg acggggagaa cgaaagtgac aggggttcc 1700
 tcataagttt tgtatgaaat atctctacaa acctcaatta gttctactct 1750
 acactttcac tatcatcaac actgagacta tcctgtctca cctacaaatg 1800
 tggaaacttt acattgttcg attttcage agactttgtt ttatTTaaatt 1850
 tttatttagtg ttaagaatgc taaattttatg tttcaatttt atttccaaat 1900
 ttctatcttg ttattgtac aacaaagtaa taaggatggt tgtcacaaaa 1950
 acaaaaactat gccttctctt tttttcaat caccagtagt atttttgaga 2000
 agacttgtga acacttaagg aaatgactat taaagtctta tttttatTT 2050
 tttcaaggaa agatggattc aaataaatta ttctgtttt gctttaaaa 2100
 aaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

Met	Trp	Leu	Lys	Val	Phe	Thr	Thr	Phe	Leu	Ser	Phe	Ala	Thr	Gly
1														
														15

Ala	Cys	Ser	Gly	Leu	Lys	Val	Thr	Val	Pro	Ser	His	Thr	Val	His
														30

Gly	Val	Arg	Gly	Gln	Ala	Leu	Tyr	Leu	Pro	Val	His	Tyr	Gly	Phe
														45

His	Thr	Pro	Ala	Ser	Asp	Ile	Gln	Ile	Ile	Trp	Leu	Phe	Glu	Arg
														60

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser
 65 70 75

Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro
 80 85 90

Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu
 95 100 105

Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu
 110 115 120

Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr
 125 130 135

Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr
 140 145 150

Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg
 155 160 165

Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser
 170 175 180

Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala
 185 190 195

Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg
 200 205 210

Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile
 215 220 225

Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu
 230 235 240

Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu
 245 250 255

Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp
 260 265 270

Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro
 275 280 285

Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp
 290 295 300

Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu
 305 310 315

Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu

320 325 330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly
335 340 345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp
350 355 360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly
365 370 375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His
380 385 390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe
395 400 405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro
410 415 420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr
425 430 435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu
440 445 450
<210> 321
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 321
gatcctgtca caaagccagt ggtgc 25

<210> 322

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 322
cactgacagg gttcctcacc cagg 24

<210> 323
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 323
ctccctctgg gctgtggagt atgtgggaa catgaccctg acatg 45

<210> 324
<211> 2397
<212> DNA
<213> Homo Sapien

<400> 324
gcaagcggcg aaatggcgcc ctccggaggt cttgcagttc ccctggcagt 50
cctggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100
acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150
tggatgatag aattttatgc cccgtggtgc cctgcttgc aaaatcttca 200
accggaatgg gaaagtttg ctgaatgggg agaagatctt gaggttaata 250
ttgcgaaagt agatgtcaca gagcagccag gactgagtg 300
ataactgctc ttcctactat ttatcattgt aaagatggt aatttaggcg 350
ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtata 400
aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450
gttctgatga gtagtatgtc agcactctt cagctatcta tgtggatcag 500
gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550
catatactgt ttttgcttta gcaactctgt tttccggact gttatttagga 600
ctctgtatga tatttgtggc agattgcctt tgtccttcaa aaaggcgcag 650
accacagcca taccataacc cttcaaaaaa attattatca gaatctgcac 700
aacctttgaa aaaagtggag gaggaacaag aggccgatga agaagatgtt 750
tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800
gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850
cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900
aagattgatc attttgtttg gtttgaagtg aactgtgact ttttgaata 950
ttgcagggtt cagtctagat tgtcattaaa ttgaagatgc tacattcaga 1000

aaacctttct aaccacttca tttaaagctga aaaaaaaaaaaa aaaaaaaaa 2397

<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

Met	Ala	Pro	Ser	Gly	Ser	Leu	Ala	Val	Pro	Leu	Ala	Val	Leu	Val
1														
													10	15

Leu	Leu	Leu	Trp	Gly	Ala	Pro	Trp	Thr	His	Gly	Arg	Arg	Ser	Asn
													20	30

Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly
													35	45

Asp	Trp	Met	Ile	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Pro	Ala	Cys	Gln
													50	60

Asn	Leu	Gln	Pro	Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp
													65	75

Leu	Glu	Val	Asn	Ile	Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly
													80	90

Leu	Ser	Gly	Arg	Phe	Ile	Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His
													95	105

Cys	Lys	Asp	Gly	Glu	Phe	Arg	Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys
													110	120

Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	Asp	Lys	Glu	Trp	Lys	Ser	Ile
													125	135

Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	Gly	Ser	Val	Leu	Met	Ser
													140	150

Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	Trp	Ile	Arg	Thr	Cys
													155	165

His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	Val	Trp	Gly	Ser
													170	180

Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly	Leu	Leu	Leu
													185	195

Gly	Leu	Cys	Met	Ile	Phe	Val	Ala	Asp	Cys	Leu	Cys	Pro	Ser	Lys
													200	210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Leu Leu

215 220 225
Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu
230 235 240
Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu
245 250 255
Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser
260 265 270
Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser
275 280
<210> 326
<211> 23
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 326
tgaggtggc aagcggcgaa atg 23

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 327
tatgtggatc aggacgtgcc 20

<210> 328
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 328
tgcagggttc agtcttagatt g 21

<210> 329
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 329
ttgaaggaca aaggcaatct gccac 25

<210> 330
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 330
ggagtcttgc agttcccttg gcagtcctgg tgctgttgct ttggg 45

<210> 331
<211> 2168
<212> DNA
<213> Homo Sapien

<400> 331
gcgagtgtcc agctgcggag acccgtata attcgtaac taattcaaca 50
aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taacccagtg 100
ggacaggcgg attggaagag cgggaaggcgc ctggccaga gcagtgtgac 150
acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200
ggtttgggt cctgagctgt gtgcaggccg aattcttac ctctattggg 250
cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300
agagtagatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350
ccaacaaaat ggaaggccttgc actagcaagt cagctgctga tgctgaggc 400
tacctggctc accctgtgaa tgcctacaaa ctggtaagc ggctaaacac 450
agactggcct gcgctggagg accttgcct gcaggactca gctgcagggt 500
ttatcgccaa cctctctgtc cagcggcagt tcttccccac tgatgaggac 550
gagataggag ctgccaaagc cctgatgaga cttcaggaca catacaggct 600
ggaccaggc acaatttcca gagggaaact tccaggaacc aagtaccagg 650
caatgctgag tgtggatgac tgctttggga tggccgcgc ggcctacaat 700
gaaggggact attatcatac ggtgttgtgg atggagcagg tgctaaagca 750

gcttcatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800
 acctcagcta tgctgtcttc cagttgggtg atctgcacccg tgccctggag 850
 ctcacccgccc gcctgctctc ccttgaccca agccacgaac gagctggagg 900
 gaatctgcgg tactttgagc agttatttggaa ggaagagaga gaaaaaacgt 950
 taacaaatca gacagaagct gagctagcaa ccccagaagg catctatgag 1000
 aggccctgtgg actacactgcc tgagagggat gtttacgaga gcctctgtcg 1050
 tggggagggt gtcaaaactga caccggtagt acagaagagg ctttctgtta 1100
 ggtaccacca tggcaacagg gccccacagc tgctcattgc ccccttcaaa 1150
 gaggaggacg agtggggacag cccgcacatc gtcaggtact acgtatgtcat 1200
 gtctgatgag gaaatcgaga ggtatcaagga gatcgcaaaa cctaaacttg 1250
 cacgagccac cgttcgttat cccaaagacag gagtcctcac tgtcgccagc 1300
 taccgggttt ccaaaagctc ctggctagag gaagatgtatg accctgttgt 1350
 ggccccagta aatcgctgga tgcagcatat cacagggtta acagtaaaga 1400
 ctgcagaatt gttacaggtt gcaaattatg gagttggggagg acagtatgaa 1450
 ccgcacttcg acttctctag gcgacccttt gacagcggcc tcaaaacaga 1500
 gggaaatagg tttagcgacgt ttcttaacta catgagtatgat gtatggctg 1550
 gtgggtgccac cgtcttcctt gatctggggg ctgcaatttg gcctaagaag 1600
 ggtacagctg tgttctggta caaccccttg cggagcgggg aaggtgacta 1650
 ccgaacaaga catgctgcct gcccctgtct tggggctgc aagtgggtct 1700
 ccaataagtg gttccatgaa cgaggacagg agttcttgag accttggta 1750
 tcaacagaag ttgactgaca tcctttctg tccttccct tcctggct 1800
 tcagcccatg tcaacgtgac agacacccctt gtatgttctt ttgtatgttc 1850
 ctatcaggct gatTTTggaa gaaatgaatg tttgtctggta gcagagggag 1900
 accataactag ggcgactcct gtgtgactga agtcccagcc ctccattca 1950
 gcctgtgcca tccctggccc caaggctagg atcaaagtgg ctgcagcaga 2000
 gtttagctgtc tagcgccctag caagggtgcct ttgtacctca ggttttttag 2050
 gtgtgagatg tttcagtgaa ccaaagttct gataccttgtt ttacatgttt 2100

gttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met	Lys	Leu	Trp	Val	Ser	Ala	Leu	Leu	Met	Ala	Trp	Phe	Gly	Val
1				5					10					15

Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met
				20					25					30

Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Lys	Glu	Leu	Val	Gln	Ser	Leu	Lys
				35					40					45

Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser
				50					55					60

Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp
				65				70						75

Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val
				80				85						90

Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu
				95					100					105

Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg
				110				115						120

Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala
				125				130						135

Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile
				140				145						150

Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser
				155				160						165

Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
				170				175						180

Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln
				185				190						195

Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Lys	Ser	Gln	Val	Leu	
				200				205						210

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg
 215 220 225
 Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His
 230 235 240
 Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu
 245 250 255
 Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu
 260 265 270
 Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro
 275 280 285
 Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys
 290 295 300
 Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His
 305 310 315
 Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu
 320 325 330
 Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met
 335 340 345
 Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys
 350 355 360
 Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr
 365 370 375
 Val Ala Ser Tyr Arg Val Ser Lys Ser Trp Leu Glu Glu Asp
 380 385 390
 Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile
 395 400 405
 Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn
 410 415 420
 Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg
 425 430 435
 Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala
 440 445 450
 Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr
 455 460 465
 Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr
 470 475 480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp
530

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 336
acactcagca ttgcctggta cttg 24

<210> 337
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 337
gggcacatga ctgacactgat ttatgcagag aaagagctgg tgcag 45

<210> 338
<211> 2789

<212> DNA
<213> Homo Sapien

<400> 338
gcagtattga gtttacttc ctccctttt tagtggaaaga cagaccataa 50
tcccagtgtg agtcaaattt attgtttcat ttattaccgt tttggctggg 100
ggtagttcc gacacccatca cagttgaaga gcaggcagaa ggagttgtga 150
agacaggaca atcttcttgg ggatgctggt cctggaaagcc agcgggcatt 200
gctctgtctt tggcctcatt gacccaggt tctctggta aaactgaaag 250
cctactactg gcctggtgcc catcaatcca ttgatccttg aggctgtgcc 300
cctggggcac ccacctggca gggccatcca ccatgcgact gagctccctg 350
ttggctctgc tgccggccagc gcttccctc atcttagggc tgtctctggg 400
gtgcagcctg agcctcctgc gggttccctg gatccagggg gagggagaag 450
atccctgtgt cgaggctgta ggggagcgag gagggccaca gaatccagat 500
tcgagagctc ggctagacca aagtgtatgaa gacttcaaac cccggattgt 550
ccccctactac agggacccca acaaggcccta caagaagggtg ctcaggactc 600
ggtacatcca gacagagctg ggctccctg agcgggttgc ggtggctgtc 650
ctgacctccc gagctacact gtccactttg gccgtggctg tgaaccgtac 700
ggtggeccat cacttccctc ggttactcta cttcaactggg cagcgggggg 750
cccgccgtcc agcagggatg caggtggtgt ctcatggga tgagcggccc 800

gcctggctca tgtcagagac cctgcgccac cttaaaaaaaaaaaaaaaaactttggggc 850
cgactacgac tggttcttca tcatacggat tgacacatata gtcaggccc 900
cccgactggc agcccttgc ggccaccta gcatcaacca agacctgtac 950
ttaggccggg cagaggagtt cattggcgca ggcgagcagg cccggtactg 1000
tcataaaaaaaaaaaaaaaa tttggctacc tggtgtcacg gagtctcctg cttcgctgc 1050
ggccacatct ggttgtgc cgaggagaca ttctcagtgc ccgtcctgac 1100
gagtggcttg gacgctgcct cattgactct ctggcgctcg gctgtgtc 1150
acagcaccag gggcagcagt atcgctcatt tgaactggcc aaaaataggg 1200
accctgagaa ggaagggaga tcggcttcc tgagtgcctt cgccgtgcac 1250
cctgtctccg aaggtaccct catgtaccgg ctccacaaac gcttcagcgc 1300
tctggagttg gagcgggctt acagtgaaat agaacaactg caggctcaga 1350
tccggAACCTT gaccgtgctg acccccgaag gggaggcagg gctgagctgg 1400
cccgttggc tccctgctcc ttccacacca cactctcgct ttgaggtgct 1450
gggctggac tacttcacag agcagcacac cttctctgt gcagatgggg 1500
ctcccaagtg cccactacag gggcttagca gggcggacgt gggtgatgcg 1550
ttggagactg ccctggagca gctcaatcg cgctatcagc cccgcctgcg 1600
cttccagaag cagcgactgc tcaacggcta tcggcgcttc gaccacgcac 1650
ggggcatgga gtacacccctg gacctgctgt tggaatgtgt gacacagcgt 1700
gggcacccggc gggccctggc tcgcagggtc agcctgctgc ggccactgag 1750
ccgggtggaa atcctaccta tgccctatgt cactgaggcc acccgagtgc 1800
agctggtgct gccactcctg gtggctgaag ctgctgcagc cccggcttcc 1850
ctcgaggcgt ttgcagccaa tgcctggag ccacgagaac atgcattgct 1900
caccctgttg ctggtctacg ggccacgaga aggtggccgt ggagctccag 1950
acccattttct tggggtaag gctgcagcag cggagttaga ggcacgggtac 2000
cctggacga ggctggcctg gtcgtgtc cgagcagagg ccccttccca 2050
ggtgcgactc atggacgtgg tctcgaagaa gcaccctgtg gacactctct 2100

tcttccttac caccgtgtgg acaaggcctg ggcccgaagt cctcaaccgc 2150
 tgcgcatga atgccatctc tggctggcag gccttcttc cagtcattt 2200
 ccaggagttc aatcctgccc tgtcaccaca gagatcaccc ccagggcccc 2250
 cgggggctgg ccctgaccgg ccctccctc ctggtgctga cccctccgg 2300
 ggggctcta tagggggag atttgaccgg caggcttctg cgaggggctg 2350
 cttctacaac gctgactacc tggcgcccg agcccgctg gcaggtgaac 2400
 tggcaggcca ggaagaggag gaagccctgg aggggctgga ggtgatggat 2450
 gtttctcc gtttctcagg gtcacccctc ttccggccg tagagccagg 2500
 gctggtgcag aagttctccc tgcgagactg cagccacgg ctcagtgaag 2550
 aactctacca ccgctgccgc ctcagcaacc tggagggct agggggccgt 2600
 gcccagctgg ctatggctc cttttagcag gagcaggcca atagcactta 2650
 gcccgcctgg gggccctaac ctcattacct ttcccttgc tgcctcagcc 2700
 ccaggaaggg caaggcaaga tggtgacag atagagaatt gttgtgtat 2750
 tttttaata tgaaaatgtt attaaacatg tttctgcc 2789

<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

Met	Arg	Leu	Ser	Ser	Leu	Leu	Ala	Leu	Leu	Arg	Pro	Ala	Leu	Pro
1														15
Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg
														30
Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
														45
Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
														60
Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
														75
Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
														90
Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala

95	100	105
Val Leu Thr Ser Arg Ala Thr Leu Ser Thr Leu Ala Val Ala Val		
110	115	120
Asn Arg Thr Val Ala His His Phe Pro Arg Leu Leu Tyr Phe Thr		
125	130	135
Gly Gln Arg Gly Ala Arg Ala Pro Ala Gly Met Gln Val Val Ser		
140	145	150
His Gly Asp Glu Arg Pro Ala Trp Leu Met Ser Glu Thr Leu Arg		
155	160	165
His Leu His Thr His Phe Gly Ala Asp Tyr Asp Trp Phe Phe Ile		
170	175	180
Met Gln Asp Asp Thr Tyr Val Gln Ala Pro Arg Leu Ala Ala Leu		
185	190	195
Ala Gly His Leu Ser Ile Asn Gln Asp Leu Tyr Leu Gly Arg Ala		
200	205	210
Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala Arg Tyr Cys His Gly		
215	220	225
Gly Phe Gly Tyr Leu Leu Ser Arg Ser Leu Leu Leu Arg Leu Arg		
230	235	240
Pro His Leu Asp Gly Cys Arg Gly Asp Ile Leu Ser Ala Arg Pro		
245	250	255
Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp Ser Leu Gly Val Gly		
260	265	270
Cys Val Ser Gln His Gln Gly Gln Gln Tyr Arg Ser Phe Glu Leu		
275	280	285
Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly Ser Ser Ala Phe Leu		
290	295	300
Ser Ala Phe Ala Val His Pro Val Ser Glu Gly Thr Leu Met Tyr		
305	310	315
Arg Leu His Lys Arg Phe Ser Ala Leu Glu Leu Glu Arg Ala Tyr		
320	325	330
Ser Glu Ile Glu Gln Leu Gln Ala Gln Ile Arg Asn Leu Thr Val		
335	340	345
Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser Trp Pro Val Gly Leu		
350	355	360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp
 365 370 375
 Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala
 380 385 390
 Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp
 395 400 405
 Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro
 410 415 420
 Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg
 425 430 435
 Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu
 440 445 450
 Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg
 455 460 465
 Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met
 470 475 480
 Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu
 485 490 495
 Leu Val Ala Glu Ala Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe
 500 505 510
 Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu
 515 520 525
 Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp
 530 535 540
 Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg
 545 550 555
 Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala
 560 565 570
 Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro
 575 580 585
 Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly
 590 595 600
 Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp
 605 610 615
 Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu
 620 625 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp
 635 640 645
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile
 650 655 660
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr
 665 670 675
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu
 680 685 690
 Ala Gly Gln Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met
 695 700 705
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val
 710 715 720
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro
 725 730 735
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu
 740 745 750
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu
 755 760 765
 Gln Glu Gln Ala Asn Ser Thr
 770

<210> 340
 <211> 1572
 <212> DNA
 <213> Homo Sapien

<400> 340
 cggagttgtg cgccaacgtg agaggaaacc cgtgcgcggc tgcgcttcc 50
 tgtccccaaag ccgttctaga cgcggaaaaa atgctttctg aaagcagctc 100
 ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
 catcatcacc tacaagctcc taacaaaagaa gatatcttga aaatttcaga 250
 ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300
 ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350
 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

gttttagtca attaatatgg acacaaatga catgtggta atgatgagaa 450
 aagcttacaa atacgcctt gataagtata gagaccaata caactggtc 500
 ttccttgcac gccccactac gtttgcatac attgaaaacc taaagtattt 550
 tttgttaaaa aaggatccat cacagcctt ctatctaggc cacactataa 600
 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650
 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700
 tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750
 cagttgcct gaaatatgct ggagtatttgc cagaaaatgc agaagatgct 800
 gatggaaaag atgtatttta taccaaatttgc gttggcattt ctattaaaga 850
 ggcaatgact tatcacccca accaggtgt agaaggctgt tgttcagata 900
 tggctgttac tttaatggc ctgactccaa atcagatgca tgtgatgatg 950
 tatgggtat accgccttag ggcatttggg catatttca atgatgcatt 1000
 ggtttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050
 agcgtgaata tgatcttgt ataggacgtg tggtgtcatt attttagta 1100
 gtaactacat atccaataca gctgtatgtt tcttttctt ttctaatttgc 1150
 gtggcactgg tataaccaca cattaaagtc agtagtacat tttaaatggc 1200
 gggtggtttt ttctttaaa acacatgaac attgtaaatg tggtggaaag 1250
 aagtgtttta agaataataa ttttgcacaa aaaactattaa taaatattat 1300
 atgtgataaa ttctaaatata tgaacattag aaatctgtgg ggcacatatt 1350
 ttgtgtgatt ggttaaaaaaa tttaacagg tctttagcgt tctaagatata 1400
 gcaaatgata tctctagttg tgaatttgcgt attaaagtaa aacttttagc 1450
 tgggtgttcc cttaacttct aatactgatt tatgttctaa gcctccccaa 1500
 gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550
 attaaagtga aagttgaaaaa at 1572

<210> 341

<211> 318

<212> PRT

<213> Homo Sapien

<400> 341

Met	Leu	Ser	Glu	Ser	Ser	Ser	Phe	Leu	Lys	Gly	Val	Met	Leu	Gly
1				5					10					15
Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile
		20							25					30
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
		35							40					45
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
			50						55					60
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
			65						70					75
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
			80						85					90
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
			95						100					105
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
			110						115					120
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
			125						130					135
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
			140						145					150
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
			155						160					165
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
			170						175					180
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
			185						190					195
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
			200						205					210
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
			215						220					225
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
			230						235					240
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile
			245						250					255
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys

<223> Synthetic Oligonucleotide Probe

<400> 345
gggtgtgatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50

<210> 346
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346
gggatgcagg tggtgtctca tgggg 25

<210> 347
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347
ccctcatgta ccggctcc 18

<210> 348
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348
ggattctaat acgactcact atagggtca gaaaagcgca acagagaa 48

<210> 349
<211> 47
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349
ctatgaaatt aaccctcact aaaggatgt cttccatgcc aaccttc 47

<210> 350
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 350
ggattctaat acgactcact atagggcgac gatgtccact ggggctac 48

<210> 351
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 351
ctatgaaatt aaccctcact aaaggacga ggaagatggg cggatgg 48

<210> 352
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 352
ggattctaat acgactcact atagggcacc cacgcgtccg gctgatt 47

<210> 353
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 353
ctatgaaatt aaccctcact aaaggacgg gggacaccac ggaccaga 48

<210> 354
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 354
ggattctaat acgactcact atagggcttg ctgcggttt tgttcctg 48

<210> 355
<211> 48

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 355
ctatgaaatt aaccctcact aaaggagct gccgatccca ctggatt 48

<210> 356
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 356
ggattctaat acgactcact atagggcgga tcctggccgg cctatg 46

<210> 357
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 357
ctatgaaatt aaccctcact aaaggagcc cggcatggt ctcagtta 48

<210> 358
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 358
ggattctaat acgactcact atagggcgga aagatggcga ggaggag 47

<210> 359
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 359
ctatgaaatt aaccctcact aaaggagcc aggccacaaa cgaaatc 48

<210> 360
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 360
ggattctaat acgactcact atagggctgt gctttcattc tgccagta 48

<210> 361
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 361
ctatgaaatt aaccctcact aaagggaggg tacaattaag gggtggat 48

<210> 362
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 362
ggattctaat acgactcact atagggcccg cctcgctct gctcctg 47

<210> 363
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 363
ctatgaaatt aaccctcact aaagggagga ttgccgcgac cctcacag 48

<210> 364
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 364

ggattctaat acgactcact atagggcccc tcctgccttc cctgtcc 47
<210> 365
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 365
ctatgaaatt aaccctcact aaaggagtg gtggccgcga ttatctgc 48

<210> 366
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 366
ggattctaat acgactcact atagggcgca gcgatggcag cgatgagg 48

<210> 367
<211> 47

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 367
ctatgaaatt aaccctcact aaagggacag acggggcaga gggagtg 47

<210> 368
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 368
ggattctaat acgactcact atagggccag gaggcgtgag gagaaac 47

<210> 369
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe
<400> 369
ctatgaaatt aaccctcact aaaggaaag acatgtcatc gggagtgg 48
<210> 370
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe
<400> 370
ggatttaat acgactcact atagggccgg gtggaggtgg aacagaaa 48
<210> 371
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe
<400> 371
ctatgaaatt aaccctcact aaaggacac agacagagcc ccataacgc 48
<210> 372
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe
<400> 372
ggatttaat acgactcact atagggccag ggaaatccgg atgtctc 47
<210> 373
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe
<400> 373
ctatgaaatt aaccctcact aaaggagta agggatgcc accgagta 48
<210> 374
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 374
ggattctaat acgactcact atagggccag ctaccgcag gaggagg 47

<210> 375
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 375
ctatgaaatt aaccctcact aaagggatcc caggtgatga ggtccaga 48

<210> 376
<211> 997
<212> DNA
<213> Homo Sapien

<400> 376
cccacgcgtc cgatcttacc aacaaaacac tcctgaggag aaagaaaagag 50
agggagggag agaaaaagag agagagagaa acaaaaaacc aaagagagag 100
aaaaaaaaatgaa ttcatctaaa tcatctgaaa cacaatgcac agagagagga 150
tgcttccttt cccaaatgtt cttatggact gttgctggta tccccatcct 200
atttctcagt gcctgtttca tcaccagatg ttttgtgaca tttcgcatct 250
ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300
ctctcctgct acaattatgg atcaggttca gtcaagaatt gttgtccatt 350
gaactggaa tattttcaat ccagctgcta cttctttct actgacacca 400
tttcctgggc gttaagttt aagaactgct cagccatggg ggctcacctg 450
gtggtatca actcacagga ggagcaggaa ttcccttcct acaagaaaacc 500
taaaatgaga gagttttta ttggactgtc agaccaggtt gtcgagggtc 550
agtggcaatg ggtggacggc acaccttga caaaagtctct gagcttctgg 600
gatgttagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650
gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700
tcaatttattt tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750

ggaaaatctc tttaagaaca gaaggcacaa ctc当地atgtg taaagaagga 800
 agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgcgc 850
 tgaacttcaa aggacttcat aagtattgt tactctgata caaataaaaa 900
 taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 997

<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

Met	Asn	Ser	Ser	Lys	Ser	Ser	Glu	Thr	Gln	Cys	Thr	Glu	Arg	Gly
1				5					10				15	

Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro
					20				25				30	

Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr
					35				40			45		

Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro
					50				55			60		

Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser
					65				70			75		

Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser
					80				85			90		

Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu
					95				100			105		

Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser
					110				115			120		

Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg
					125				130			135		

Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp
					140				145			150		

Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp
					155				160			165		

Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala
					170				175			180		

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
185 190 195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile
200 205 210

Asn Pro Leu Asn Lys Gly Lys Ser Leu
215

<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

ttcagcttct gggatgtagg g 21

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg 49

<210> 381

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

gcagatttg aggacagcca cctcca 26

<210> 382
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 382
ggccttgcag acaaccgt 18

<210> 383
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 383
cagactgagg gagatccgag a 21

<210> 384
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 384
cagctgccct tccccaaacca 20

<210> 385
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 385
catcaagcgc ctctacca 18

<210> 386
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 386

cacaaaactcg aactgcttct g 21
<210> 387
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 387
ggccatcac agtcacct 18

<210> 388
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 388
gggatgttgtt gaacacagaa ca 22

<210> 389
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 389
tgccagctgc atgctgccag tt 22

<210> 390
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 390
cagaaggatg tccccgtggaa 20

<210> 391
<211> 17
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe
<400> 391
gcccgtgtcc actgcag 17

<210> 392
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 392
gacggcatcc tcagggccac a 21

<210> 393
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 393
atgtcctcca tgcccacgcg 20

<210> 394
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 394
gagtgcgaca tcgagagtt 20

<210> 395
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 395
ccgcagcctc agtgatga 18

<210> 396
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 396
gaagagcaca gctgcagatc c 21

<210> 397
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 397
gaggtgtcct ggctttggta gt 22

<210> 398
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 398
cctctggcgc ccccaactcaa 20

<210> 399
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 399
ccaggagagc tggcgatg 18

<210> 400
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 400
gcaaattcag ggctcactag aga 23

<210> 401
<211> 29

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 401
cacagagcat ttgtccatca gcagttcag 29

<210> 402
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 402
ggcagagact tccagtcact ga 22

<210> 403
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 403
gccaagggtg gtgttagata gg 22

<210> 404
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 404
caggccccct tgatctgtac ccca 24

<210> 405
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 405
gggacgtgct tctacaagaa cag 23

<210> 406
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 406
caggcttaca atgttatgtat cagaca 26

<210> 407
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 407
tattcagagt tttccattgg cagtgccagt t 31

<210> 408
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 408
tctacatcag cctctctgcg c 21

<210> 409
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 409
cgatcttctc cacccaggag cg 23

<210> 410
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 410

gccaggcctc acattcgt 18
<210> 411
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 411
ctccctgaat ggcagcctga gca 23

<210> 412
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 412
aggtgtttat taagggccta cgct 24

<210> 413
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 413
cagagcagag ggtgccttg 19

<210> 414
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 414
tggcgagtc ccctcttggc t 21

<210> 415
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 415
ccctgttcc ctatgcata ct 22

<210> 416
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 416
tcaacccctg accctttcct a 21

<210> 417
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 417
ggcagggac aagccatctc tcct 24

<210> 418
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418
gggactgaac tgccagttc 20

<210> 419
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 419
gggcctaacc ctcattaccc tt 22

<210> 420
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 420
tgtctgcctc agccccagga agg 23

<210> 421
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 421
tctgtccacc atcttgccctt g 21

<210> 422
<211> 3554
<212> DNA
<213> Homo Sapien

<400> 422
gggactacaa gccgcgcgc gctgccgctg gcccctcagc aaccctcgac 50
atggcgctga ggccgcacc gcgactccgg ctctgcgctc ggctgcctga 100
cttcttcctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150
tcaaataccag caatcgaacc ccagtggta aggaatttga aagtgtggaa 200
ctgtcttgca tcattacgga ttgcgcagaca agtgacccca ggatcgagtg 250
gaagaaaatt caagatgaac aaaccacata tgtgttttt gacaacaaaa 300
ttcagggaga cttggcggtt cgtgcagaaa tactgggaa gacatccctg 350
aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400
cgttgctcga aatgacccgca aggaaattga tgagattgtg atcgagttaa 450
ctgtgcaagt gaagccagt accccctgtct gtagagtgcc gaaggctgta 500
ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550
ccggcctcac tacagctggt atcgaaatga tgttaccactg cccacggatt 600
ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650
acaggcactt tggtgttcac tgctgttcac aaggacgact ctggcagta 700
ctactgcatt gcttccaatg acgcaggctc agccaggtgt gaggagcagg 750

agatggaagt ctatgacctg aacattggcg gaattattgg gggggttctg 800
gttgccttg ctgtactggc cctgatcacg ttggcatct gctgtgcata 850
cagacgtggc tacttcatca acaataaaaca ggatggagaa agttacaaga 900
acccaggaa accagatgga gttaactaca tccgcactga cgaggaggc 950
gacttcagac acaagtcatc gtttgtatc tgagaccgc ggtgtggctg 1000
agagcgcaca gagcgcacgt gcacataacct ctgctagaaa ctcctgtcaa 1050
ggcagcgaga gctgatgcac tcggacagag ctagacactc attcagaagc 1100
tttcgtttt gccaaagtt gaccactact cttcttactc taacaagcca 1150
catgaataga agaattttcc tcaagatgga cccggtaaat ataaccacaa 1200
ggaagcgaaa ctgggtgcgt tcactgagtt gggttcctaa tctgtttctg 1250
gcctgattcc cgcatgagta ttagggtgat cttaaagagt ttgctcacgt 1300
aaacccccgt gctggggccct gtgaagccag catgttcacc actggtcgtt 1350
cagcagccac gacagcacca tgtgagatgg cgaggtggct ggacagcacc 1400
agcagcgcac cccggcgaaa acccagaaaa ggcttcttac acagcagcct 1450
tacttcatcg gcccacagac accaccgcag tttcttctta aaggctctgc 1500
tgatcggtgt tgcagtgtcc attgtggaga agcttttgg atcagcattt 1550
tgtaaaaaca accaaaatca ggaaggtaaa ttgggtgctg gaagagggat 1600
ttgcctgag gaaccctgct tgtccaacag ggtgtcagga tttaaggaaa 1650
acttcgtct taggctaagt ctgaaatggt actgaaatat gctttctat 1700
gggtcttggatt tattttataa aattttacat ctaaattttt gctaaggatg 1750
tattttgatt attgaaaaga aaatttctat taaaactgta aatatattgt 1800
catacaatgt taaataacct attttttaa aaaagttcaa cttaaggtag 1850
aagttccaag ctactagtgt taaattggaa aatatcaata attaagagta 1900
ttttacccaa ggaatcctct catggaagtt tactgtgatg ttccctttct 1950
cacacaagtt ttagcctttt tcacaaggaa actcatactg tctacacatc 2000
agaccatagt tgcttaggaa acctttaaaa attccagtttta agcaatgtt 2050

aaatcagttt gcatctcttc aaaagaaaacc tctcaggtta gcttgaact 2100
gcctttccct gagatgacta ggacagtctg tacccagagg ccacccagaa 2150
gccctcagat gtacatacac agatgccagt cagctcctgg ggttgegcca 2200
ggcgcccccg ctctagctca ctgttgccctc gctgtctgcc aggaggccct 2250
gccatccttg ggccctggca gtggctgtgt cccagtgagc tttactcacg 2300
tggcccttgc ttcatccagc acagctctca ggtggcact gcagggacac 2350
tggtgtcttc catgttagcgt cccagctttg ggctcctgta acagacctct 2400
ttttggttat ggatggctca caaaataggg ccccaatgc tattttttt 2450
ttttaagttt gtttaattat ttgttaagat tgtctaaggc caaaggcaat 2500
tgcgaaatca agtctgtcaa gtacaataac attttaaaaa gaaaatggat 2550
cccactgttc ctcttgcca cagagaaagc acccagacgc cacaggctct 2600
gtcgcatttc aaaacaaacc atgatggagt ggccggccagt ccagccttt 2650
aaagaacgtc aggtggagca gccaggtgaa aggccctggcg gggaggaaag 2700
tgaaacgcct gaatcaaaag cagtttcta atttgactt taaattttc 2750
atccggccgga gacactgctc ccatttgtgg ggggacattha gcaacatcac 2800
tcagaaggcct gtgttcttca agagcaggtg ttctcagcct cacatgcct 2850
gccgtgctgg actcaggact gaagtgctgt aaagcaagga gctgctgaga 2900
aggagcactc cactgtgtgc ctggagaatg gctctcacta ctcacccctgt 2950
cttcagctt ccagtgtctt gggttttta tactttgaca gcttttttt 3000
aattgcatac atgagactgt gttgactttt tttagttatg tgaaacactt 3050
tgccgcaggg cgcctggcag aggcaggaaa tgctccagca gtggctcagt 3100
gctccctgggt gtctgctgca tggcatcctg gatgcttagc atgcaagttc 3150
*
cctccatcat tgccacccctg gtagagaggg atggctcccc accctcagcg 3200
ttggggattc acgctccagc ctccttctt gttgtcatag tgatagggta 3250
gccttattgc cccctttct tataccctaa aaccttctac actagtgcct 3300
tgggaaccag gtctgaaaaa gtagagagaa gtgaaaagtag agtctggaa 3350
gtagctgcct ataactgaga ctagacggaa aaggaatact cgtgtatTTT 3400

aagatatgaa tgtgactcaa gactcgaggc cgatacgagg ctgtgattct 3450
 gccttggat ggatgttgct gtacacagat gctacagact tgtactaaca 3500
 caccgtaatt tggcatttgt ttaacctcat ttataaaagc ttcaaaaaaa 3550
 ccca 3554

<210> 423
<211> 310
<212> PRT
<213> Homo Sapien

<400> 423

Met	Ala	Leu	Arg	Arg	Pro	Pro	Arg	Leu	Arg	Leu	Cys	Ala	Arg	Leu
1					5				10					15

Pro	Asp	Phe	Phe	Leu	Leu	Leu	Phe	Arg	Gly	Cys	Leu	Ile	Gly	
				20				25					30	

Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu
				35					40				45	

Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr
				50				55					60	

Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Ile	Gln	Asp	Glu	Gln	Thr	
				65				70					75	

Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly
					80				85				90	

Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val
					95				100				105	

Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg
					110				115				120	

Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val
					125				130				135	

Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val
					140				145				150	

Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Gly	
					155				160				165	

His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu
					170				175				180	

Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe
					185				190				195	

His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His
200 205 210

Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala
215 220 225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu
230 235 240

Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val
245 250 255

Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly
260 265 270

Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro
275 280 285

Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly
290 295 300

Asp Phe Arg His Lys Ser Ser Phe Val Ile
305 310